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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 15:47:39 ; Search time 313.62 Seconds  
(without alignments)  
7887.743 Million cell updates/sec

Title: US-09-292-411a-1  
Perfect score: 771  
Sequence: 1 atcttaaatcttgaaacaa.....gattccacgcaataataaa 771

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2138461 seqs, 1604250230 residues

Total number of hits satisfying chosen parameters: 4276922

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA\_New:\*  
1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq2:\*  
8: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	767.6	99.6	774	7 US-10-089-019-11	Sequence 11, Appl
2	761	98.7	916	7 US-10-138-701-5	Sequence 5, Appl
3	325.6	42.2	777	8 US-60-360-039-40175	Sequence 40175, A
4	286.8	37.2	783	8 US-60-360-039-41051	Sequence 41051, A
5	247.8	32.1	810	8 US-60-360-039-41383	Sequence 41383, A
6	224.6	29.1	792	8 US-60-360-039-42526	Sequence 42526, A
7	222.2	28.8	780	8 US-60-360-039-43741	Sequence 43741, A
8	191.6	24.9	753	8 US-60-360-039-42031	Sequence 42031, A
9	182.2	23.6	837	8 US-60-360-039-26327	Sequence 26327, A
10	150.6	19.5	786	8 US-60-360-039-24075	Sequence 24075, A
11	140	18.2	889	5 US-09-882-227-493	Sequence 493, App
12	137.8	17.9	786	8 US-60-360-039-44878	Sequence 44878, A
13	133	17.3	768	8 US-60-360-039-43253	Sequence 43253, A
14	129.2	16.8	783	8 US-60-360-039-35437	Sequence 35437, A
15	129.2	16.8	783	8 US-60-360-039-37978	Sequence 37978, A
16	129.2	16.8	783	8 US-60-360-039-38173	Sequence 38173, A
17	129.2	16.8	783	8 US-60-360-039-38557	Sequence 38557, A
18	127	16.5	780	8 US-60-360-039-33737	Sequence 33737, A
19	122.6	15.9	819	8 US-60-360-039-35974	Sequence 35974, A
20	121.8	15.8	789	7 US-10-089-019-23	Sequence 23, Appl
21	121.8	15.8	789	8 US-60-360-039-24499	Sequence 24499, A
22	119.8	15.5	792	8 US-60-360-039-37477	Sequence 37477, A
23	119.2	15.5	762	8 US-60-360-039-44299	Sequence 44299, A
24	118.4	15.4	762	8 US-60-360-039-41596	Sequence 41596, A
25	112.6	14.6	858	8 US-60-360-039-23801	Sequence 23801, A

ALIGNMENTS

RESULT 1

US-10-089-019-11  
; Sequence 11, Application US/10089019  
; GENERAL INFORMATION:  
; APPLICANT: DEMWOLF, WALTER E. JR  
; APPLICANT: KALLENDER, HOWARD  
; APPLICANT: LONSDALE, JOHN T.  
; TITLE OF INVENTION: METHODS FOR MAKING AND USING FATTY ACID  
; TITLE OF INVENTION: SYNTHESIS PATHWAY REAGENTS  
; FILE REFERENCE: GM50068  
; CURRENT APPLICATION NUMBER: US/10/089,019  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/US00/29451  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: 60/161,775  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-089-019-11

Query Match	99.6%	Score 767.6;	DB 7;	Length 774;
Best Local Similarity	100.0%	Pred. No. 1.1e-179;		
Mismatches	768;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps	0;			
QY	4	ttaaattcttgaaacaaacacatgtcatcgtggaatcgtaataagcgtattgct	63	
Db	7	ttaaattcttgaaacaaacacatgtcatcgtggaatcgtaataagcgtattgct	66	
QY	64	tttggtgcgtctaaagtcttagatcaattagtgcttaattatttaccgtaaa	123	
Db	67	tttggtgcgtctaaagtcttagatcaattagtgcttaattatttaccgtaaa	126	
QY	124	gaacgtacgcgttaaagagcttgaaaaattattagaacaaattaaacacagagcgac	183	
Db	127	gaacgtacgcgttaaagagcttgaaaaattattagaacaaattaaacacagagcgac	186	
QY	184	ttatatacaattgattgttcaaacgcatgaagaggttatttaattgttttgagcaaatggt	243	
Db	187	ttatatacaattgattgttcaaacgcatgaagaggttatttaattgttttgagcaaatggt	246	
QY	244	aaagatgttgcccaattgattgtgtatcatcattgcatttgcatttaataatgaagac	303	
Db	247	aaagatgttgcccaattgattgtgtatcatcattgcatttgcatttaataatgaagac	306	

Qy 304 ttacgcgacgctttctgaaacttcacgtgaaggcttcttctgttagctcaagacattagt 363  
Db 307 ttacgcgacgctttctgaaacttcacgtgaaggcttcttctgttagctcaagacattagt 366  
Qy 364 tcttactcattaaacatttggtgcacatgaagctaaataaatttaagccagaagggtgtagc 423  
Db 367 tcttactcattaaacatttggtgcacatgaagctaaataaatttaagccagaagggtgtagc 426  
Qy 424 attgtgcaacaacattattaggtgcaaatcgcagttcgaataataataatttaagctggt 483  
Db 427 attgtgcaacaacattattaggtgcaaatcgcagttcgaataataataatttaagctggt 486  
Qy 484 gttgctaaagcagcttagaagcaaatgttaaatatttagcattagcattaggtctctgat 543  
Db 487 gttgctaaagcagcttagaagcaaatgttaaatatttagcattagcattaggtctctgat 546  
Qy 544 aatttcgcgttaattgaatttcagctgctgcacatccgtagcattaaagtgcaaaagggtg 603  
Db 547 aatttcgcgttaattgaatttcagctgctgcacatccgtagcattaaagtgcaaaagggtg 606  
Qy 604 ggtggttcaatacaattcttaagaaatcgaagacgctgcacctttaaaacgtaaacgtt 663  
Db 607 ggtggttcaatacaattcttaagaaatcgaagacgctgcacctttaaaacgtaaacgtt 666  
Qy 664 gatcaagtagaagtaggttaaacagcggcttacttrttaagtgacttatcaagtggcgtt 723  
Db 667 gatcaagtagaagtaggttaaacagcggcttacttrttaagtgacttatcaagtggcgtt 726  
Qy 724 acaggtgaaatattcatgtagatagcggattccacgcaataataa 771  
Db 727 acaggtgaaatattcatgtagatagcggattccacgcaataataa 774

RESULT 2  
US-10-138-701-5  
; Sequence 5, Application US/10138701  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides  
; FILE REFERENCE: PB484  
; CURRENT APPLICATION NUMBER: US/10/138,701  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: US/09/512,255A  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/098,964  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: US 60/009,861  
; PRIOR FILING DATE: 1996-01-05  
; PRIOR APPLICATION NUMBER: PCT/ US99/19726  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: US 08/956,171  
; PRIOR FILING DATE: 1997-10-20  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 916  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-138-701-5

Query Match 98.7%; Score 761; DB 7; Length 916;  
Best Local Similarity 99.1%; Pred. No. 4.8e-178;  
Matches 764; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 atgttaaatcttgaacaaacatatgtcatcattggaatcgtaataagcgttagtatt 60  
Db 96 atgttaaatcttgaacaaacatatgtcatcattggaatcgtaataagcgttagtatt 155  
Qy 61 gcttttggtgcgtaaagtttagatcaattaggtgctaaattagttatttacttaacgt 120  
Db 156 gcttttggtgcgtaaagtttagatcaattaggtgctaaattagttatttacttaacgt 215

Qy 121 aaagaacgtagccgttaaagagcttgaaataattatttagaacaattaaatacaccagaagcg 180  
Db 216 aaagaacgtagccgttaaagagcttgaaataattatttagaacaattaaatacaccagaagcg 275  
Qy 181 cacttatatacaaatgtgcttcaaaagcagatgaagagggtatttaattggttttgagcaaat 240  
Db 276 cacttatatacaaatgtgcttcaaaagcagatgaagagggtatttaattggttttgagcaaat 335  
Qy 241 ggtaaagtggtgcaaatattgattgatttatcatcattcaatcgcaatttgcataatggaa 300  
Db 336 ggtaaagtggtgcaaatattgattgatttatcatcattcaatcgcaatttgcataatggaa 395  
Qy 301 gacttacgcggacgcttttctgaaacttcacgtgaaggcttcttctgttagctcaagacatt 360  
Db 396 gacttacgcggacgcttttctgaaacttcacgtgaaggcttcttctgttagctcaagacatt 455  
Qy 361 agttctactcattaaacaatttggtgctcatgaagctaaataaatttaagccagaagggtggt 420  
Db 456 agttctactcattaaacaatttggtgctcatgaagctaaataaatttaagccagaagggtggt 515  
Qy 421 agcattgttgcacaacacatatatttaggtgctgaattcgcagttcgaataatttaattgtgag 480  
Db 516 agcattgttgcacaacacatatatttaggtgctgaattcgcagttcgaataatttaattgtgag 575  
Qy 481 ggtgtgctaaagcagcttagaagcaaatgttaaatatttagcatttagacttagtctct 540  
Db 576 ggtgtgctaaagcagcttagaagcaaatgttaaatatttagcatttagacttagtctca 635  
Qy 541 gataatattcgcgttaattgcaatttcagctggtccaaatccgtacatttaagtgcaaaaggt 600  
Db 636 gataatattcgcgttaattgcaatttcagctggtccaaatccgtacatttaagtgcaaaaggt 695  
Qy 601 gtcggtggttccatacaattcttaagaaatcgaagacgctgcacctttaaaacgtaac 660  
Db 696 gtcggtggttccatacaattcttaagaaatcgaagacgctgcacctttaaaacgtaac 755  
Qy 661 gttgatcaagtagaagtaggttaaaacagcggcttacttrttaagtgacttatcaagtgcc 720  
Db 756 gttgatcaagtagaagtaggttaaaacgcttacttacttatttaagtgatttatcaagtgcc 815  
Qy 721 gttacaggtgaaataattcatgtagatagcggattccacgcaataataa 771  
Db 816 gttacaggtgaaataattcatgtagatagcggattccacgcaataataa 866

RESULT 3  
US-60-360-039-40175  
; Sequence 40175, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 40175  
; LENGTH: 777  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
US-60-360-039-40175

Query Match 42.2%; Score 325.6; DB 8; Length 777;  
Best Local Similarity 64.2%; Pred. No. 1.1e-70;  
Matches 487; Conservative 1; Mismatches 270; Indels 0; Gaps 0;  
Qy 1 atgttaaatcttgaacaaacatatgtcatcattggaatcgctaaataagcgttagtatt 60

Db 16 aggaactattacaagggaaaacattgtgttatggcgctgcgaacaaaagtatt 75  
QY 61 gctttgtgtgtcctaaagtatttagataattaggtgctcaaatatttagtatttaccgt 120  
Db 76 gcatggggaatagtcgtcttgcataatgcatgagtgcaaaatttaattacatatgca 135  
QY 121 aaagaacgtagcgttaagaagcttgaaataattattagaacaattaaatcaacagaagcg 180  
Db 136 ggagaacgtttgaagaacgttcgtgaattagcgacacatttagaaggacaagaatca 195  
QY 181 cacttatatacaattgatgttcaagcgatgaaggggttatataatgttttagcaaaatt 240  
Db 196 ctgtattacccttgatgtgaacgaatgatgaggaaacttacagcttgcctttgaaacaatt 255  
QY 241 ggttaagaattgttggcaaatattgatgttatcatcattcattcgcatttgccttaattggaa 300  
Db 256 aaacaagaagtaggtactattcacggttagcacattgtattgcttttgcataatcgcat 315  
QY 301 gacttacgagcgtctttctgaaacttcacgtgaagcgttcttctgttagctcaagacatt 360  
Db 316 gacttaaaaggtgaattttagatactctcgcgtgagatttttacttgcacaaaatt 375  
QY 361 agtttacttacttaacaattgtgctcatgaagctaaataattaaatgcagaagtggt 420  
Db 376 agcgcaattctcttaacagcttagcaagagcgaagcgaagagtaattgacagaagcgga 435  
QY 421 agcattgttgcacaacataatttagtggcggaattcgcagttcacaataattatattgtgatg 480  
Db 436 aatattttaaatacaatacacttggcgcgagcgttggtaaaattataacgttatg 495  
QY 481 ggtgtgctaaagcagcgttagaagcaaatgttaaatatttagcatttagcttaggtcct 540  
Db 496 ggtgttgcgaagccttcatttagaagcagcgtgaataatttagcgaacgatttagtcaa 555  
QY 541 gataatattcgtgttaattcaatttcagctgttccaaatccgtacatttaagtgcgaaggt 600  
Db 556 cagcgtattcgtgttaacgctattctgcaggaccaattcgtacgttatctgcaaaagt 615  
QY 601 gttgggtgttcaatacaatacttcaagaatacgaagcgtgcacctttaaacaagtaac 660  
Db 616 gtagcgatttcaactcaatttagaagaaattgaggagcgcacacacttgctgata 675  
QY 661 gttgataagtagaagtagttaaagcagcggcttactttrtaagtgaacttatcaagtgc 720  
Db 676 acaacgcaagaaggttgcgatacagcagtgatttcttacttactttagcagcgggt 735  
QY 721 gttacaggtgaaataattcattcatagatagcggaattcca 758  
Db 736 gtaacaggagaaacattcatctgtgattcagggtatca 773

## RESULT 4

US-60-360-039-41051  
; Sequence 41051, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 41051

; LENGTH: 783

; TYPE: DNA

; ORGANISM: Bacillus halodurans

US-60-360-039-41051

Query Match 37.2%; Score 286.8; DB 8; Length 783;  
Best Local Similarity 61.8%; Pred. NO. 4e-61;  
Matches 456; Conservative 0; Mismatches 282; Indels 0; Gaps 0;

QY 22 acatatgtcatcatcgaatcgtaataagcgtagtagtattgcttttggctgcgtaaagt 81  
Db 28 acatatgtgtcatggcgctgcgaataagcgtagtagtattgcttttggctgcgtaaagt 87  
QY 82 ttatgataataggtgctaaattagtagtatttacttaccgttaagaagcgttagcgttaagag 141  
Db 88 ctagccaattgcagggaacaggcgtgatttttacgtatgcgggagaacgacttgagaaaaat 147  
QY 142 ctggaataattattagaacaattaaatcaaccagaagcgcacttatatacaaaattgatt 201  
Db 148 gttagaggttagtgtaaacgcttagagcgtgtagtgcacacctgatttagagtgtagtg 207  
QY 202 caaagcgatgaagaggttatttaattggtttttagcaaaattggttaagaattggtgcaaat 261  
Db 208 acaagtgtatgaagcgtttgaagcaacatttgcgagcatcaagaggaagcgaattggcaaat 267  
QY 262 gatgtgtatatacatcattcgaatcgcatttgcataatggaagcacttagcgcgacgtttct 321  
Db 268 catggttaggtcactgcgtcgttttgcataataagagaggttagaaggggagtattta 327  
QY 322 gaacttcacgtgaagcgttctttagctcaagacatttagtcttacttactcatttaacaatt 381  
Db 328 aatacgcactgcgtgatttttatttagctcacaataatttagtcatactctttagacggt 387  
QY 382 gttgctcatgaagcgtcaaaaatttaagcagaaggtggttagcatttggcaacaacatat 441  
Db 388 gtggcgaagcgtcccgctcatgaacgaaggaaggaagcgttaacacttactat 447  
QY 442 ttatgtggcgaaattcgcagttcaaaattataatgtatggtgtgttgcataaagcgactta 501  
Db 448 ttaggcgttgaaagaattgtccgttaataatcatttatttggcgcagcagggcgtctct 507  
QY 502 gaagcaaatgttaattatttagcatttagccttagctgctgataataattcgcgttaagtca 561  
Db 508 gacgcagcgtgaagtagtatttagcaaacgacttctggcaaggaacacattcgcgttaacgct 567  
QY 562 attcagcgtgctccatccgtacattaaagtgcgaaggtggtggttgggttttcaatacaatt 621  
Db 568 attcgcgtggaacgtaccgcaccttgcgccaaaggaatcgcggttcaatgacgtc 627  
QY 622 cttaagaataatcgaagcgtgcacctttaaaccgttaacgttgcataagtagagtaggt 681  
Db 628 ttaagagaatacgaagagcgtgcaccactccgcgaacacactacgaagaagtaggg 687  
QY 682 aaaaacgcggttacttrttaagtgcatttatcaagtggcgttacaggtgaaaaattcat 741  
Db 688 gatactgcatgttctctcatgtagtgcctttcaagaggaatcagagggaaattttacac 747  
QY 742 gtatagacgggattccac 759  
Db 748 gtatagacgggataaac 765

## RESULT 5

US-60-360-039-41383

; Sequence 41383, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374



Qy	9	tcttgaaacacaaacatatgtcatcatcgtggaaatcgtcctaatacgtcgtagttattgctctttgg	68
Db	6	tttagagggttaaaaaattgttatcctgggtgtgtcacaataaaatctattgcttgggg	65
Qy	69	tgtcgtcaaaagttttagatcaattaggctgctaaattagttattactacgtctaaagaacg	128
Db	66	ctgtctaaagcaatgaaagatcaaggctgcaacatttaatttacttaccaaaatgaacg	125
Qy	129	tagccgtaaagagcttgaaaaattattagacaacattataatcaaccagaagcgcacttata	188
Db	126	aa-----tggaaaaacaattagctaaattggctggaaccagaagatttgtcat	173
Qy	189	tcaaatgatgttcgaagcgatgaagaggttatttaattggttttggacaaattggttaaga	248
Db	174	tgaatgtagtaactctctgatgaatctatgcgcgtcttttggctacaaatggagcg	233
Qy	249	tgttggcaattattgattggtgtatcatcctcaatcgcaatttgcctaaatggaagacttaag	308
Db	234	tgtcggtaaaattgacggacttgttcatgccattgcttactctaaaaagaagagcttgg	293
Qy	309	cggacgctttctgaaacttcaogtgaagcgtctcttgtttagctcagaacattagttcttta	368
Db	294	tgggaattgtacagatattctctgcgattggttatgccttgcctcaagatttccagctta	353
Qy	369	ctcatcaacaatttgcctcatgaagctataaaataaagtcgaaggtgggtagcattgt	428
Db	354	cagcttgcctgtgttctctaaagcagcaaacacattgcttcaaaaaggttctggtatcgt	413
Qy	429	tgcacaacatatattagttggcgcaattcgcagtttcaaaattataatgtgatgggtgttgc	488
Db	414	aacttgaacttaccatgggttcagctctgcattcttcctaacatacaatgttatgggaattgc	473
Qy	489	taaagcagcttagaagcaaaatgttaaatatttagcatttagaacttaggtcctcataatat	548
Db	474	taaagcagctcttgaaactacagtttgttatcttctgtctgtaaatggcatataggtgt	533
Qy	549	tccggttaaatgcaatttccagctgtgtccaaatccgtcacatttaagtgcgaaggttgggtg	608
Db	534	tcatgtgaacggaattcttcgaggagcaattaaacaacttgcggtttctcgagatttcagg	593
Qy	609	tttcaatacaattctttaaagaaatcgaagagcgtgcacottttaaaacgttaacgttgtatca	668
Db	594	ttaacaagatttgattaaagaatcttcgacgcgtcacagctgattgtcttggttgaacaat	653

QY 669 agtagaagtagtagtaaaacagcggcgttactttrttaagtgaacttatcaaatgaagtggtacagg 728  
Db 654 tgatgatgtgggtcaaaactgcgccttctctgttagcccaactgctcagggtgtcatgg 713  
QY 729 tgaataatcatgtagatagcggattccacgcaatataa 768  
Db 714 tgatatcgtttatgtgataaagggttcattcaataa 753

RESULT 9  
US-60-360-039-26327  
; Sequence 26327, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 26327  
; LENGTH: 837  
; TYPE: DNA  
; ORGANISM: Synechocystis sp.  
US-60-360-039-26327

Query Match 23.6%; Score 182.2; DB 8; Length 837;  
Best Local Similarity 53.4%; Pred. No. 2.5e-35;  
Matches 404; Conservative 1; Mismatches 349; Indels 3; Gaps 1;

QY 1 atgttaaatcttgaaacacacatatgtcatcgtggaatcgtaataaagcgtagtatt 60  
Db 61 atgttagatctcagcggcaagcagcccttgttacccgcatcgccaataatcgctccatt 120  
QY 61 gcttttggtgcgttaaaagttagatcaattagtgctgtataattagttacttaccgt 120  
Db 121 gcttggtgcatgcccacacactacacagccggcggtgtaattggttagttattt 180  
QY 121 aaagacatagcgttaagagcttgaaataattattagacaataaaa---tcaaccagaa 177  
Db 181 ccagatgagaagggcagatttgaaagaaagtgcgggagtgaccagcccttgcacct 240  
QY 178 gcgcacttatcaaatgatgttcaaaagcagatgaagaggttattaaatggtttgagcaa 237  
Db 241 accctcgcttgcgggggacgtacagacgatgccagggtggatgccctgttccatagc 300  
QY 238 atggtaaaagattgtggcaatattgatgggtgtatattcaatcgcatttgcataatg 297  
Db 301 gttaaagaaaattgggcaaaactcgatatttgcattccttagccttgcgcgacaag 360  
QY 298 gaagacttaacgcgcgtctttctgaaacttcaacgtgaagcgtcttctgttagctcaagac 357  
Db 361 tccggtttgacgggaattataccgatattcccaagggaagccttttagtcaagcaatggaa 420  
QY 358 attagttctactcattaaacattgtggtcattgaagctaaataaattaatccgaaggt 417  
Db 421 attgacacctattccctggcggttggctcgggggcaaaccccttgatgaccaatggc 480  
QY 418 ggtagcattgttgcaacacacataatttagtggcgaattcgcagttcgaataataatgtg 477  
Db 481 ggtagcattacacctgaacttacttggcggcggtgaaggttattcccaactacaacctg 540  
QY 478 atgggtgtgtgaagcagcttagaagcaaatgttaaatattbagcattagattaggt 537  
Db 541 atgggggtggcgaagggcggctctggaatgactgtgcgttatctggcgcgagaattgggg 600  
QY 538 cctgataatctcgcttaactgaatttcagctgttccatccgtacattaaagtgcacaaa 597

Db 601 ccccaaaatattcgtgttaatttcttcgctggcccatcgcgacccctggtcttctcg 660  
QY 598 ggttggtggtttcaatacaattcttaagaataaagaaacgaagagcgtgcacctttaaaact 657  
Db 661 gcgggtgggggcaattttggatattgattcccatgtggaagaggtggcaccactaaagcgt 720  
QY 658 aacgttgatcagtagaagtaggttaaaacagcgggttactttrttaagtgaacttatcaagt 717  
Db 721 accgtcacccaaacggaagtggaatacacagcggcttctcctggccagtgacctttccagt 780  
QY 718 ggcgttacaggtgaaataattcatatagatagcggat 754  
Db 781 ggcattaccggacaataattatctacgtcgtcttctggtct 817

RESULT 10  
US-60-360-039-24075  
; Sequence 24075, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 24075  
; LENGTH: 786  
; TYPE: DNA  
; ORGANISM: Xenorhabdus nematophilus  
US-60-360-039-24075

Query Match 19.5%; Score 150.6; DB 8; Length 786;  
Best Local Similarity 52.3%; Pred. No. 1.5e-27;  
Matches 383; Conservative 1; Mismatches 340; Indels 9; Gaps 2;

QY 27 tgtcatcctgggaatcgcttaataagcgttagtattggttgcgttaagattttaga 86  
Db 27 tctaatcctggcgtgcgcagcaaaactgtctattgcttgaattggcgaagcaatgca 86  
QY 87 tcaattagtgctaaattagttatttacttaccgttaaaagacgtagccgtaaagagcttga 146  
Db 87 cgacaagggtgcagaactggcttttaccctaccagaatgacaaaattgaaacctcgtgtga 146  
QY 147 aaattattagaacaaattaaatcaaccagagcgcacttatcatcaaatgttgttcaag 206  
Db 147 gaattcgcagcatctcgtgaattcacaacatcgttctgcacgtgcagctggctc-----a 200  
QY 207 cgatgaagaggttattaatggtttttgagcaaaattggtaaaagatgttgcaatattgctgg 266  
Db 201 agatgaagtagtcacacacattgttctgttgaactgggtggaagtattggcgaatattcgatgg 260  
QY 267 tgtatattcaatcgcatttgcgttaaatatggaagacttac---gcggacgttttttga 323  
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QY 324 aacttcactggaaggcttctgttagctcaagacatttgcgttacttactattcaacaattgt 383  
Db 321 cgtcagcgtgaaaggtttcaaaaatagcacatgatcatcagcgcatcacacttcgtgcgcat 380  
QY 384 ggtcctgaagactaaaaaattaaatgcccagaaggtggttagcattgttgcaacaacatattt 443  
Db 381 ggcaaaagcgtgctgtagtatgctgaatccctgactcagcgtgctgaacttttaagctattt 440  
QY 444 aggtggcgaaattccagcttcaaaaattaaatgtagtgggttcttgcataaagcgagcttaga 503  
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[illegible]

RESULT 15  
US-60-360-039-37978  
US-60-360-039-37978, Application US/603600039  
; SEQUENCE INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 37978  
; LENGTH: 783  
; TYPE: DNA  
; ORGANISM: Agrobacterium tumefaciens  
US-60-360-039-37978

Query Match	16.8%;	Score 129.2;	DB 8;	Length 783;	
Best Local Similarity	50.3%;	Pred. No. 2.9e-22;			
Matches 370;	Conservative	1;	Mismatches 359;	Indels 6;	Gaps
Qy	29	tcatacgtggaatcgctaataaagcgtagttatgcttttggctgcgtcaaatgttttagatc	88		
Db	26	tcatacgtggcgctgcgcataaaccgttcaatcgcttggggcattgcaaaaggcctgcgcgg	85		
Qy	89	aattagtgctcaaatattagttatttacttaccgttaagaacgtagccgttaagaagccttga	148		
Db	86	atgcaggctgggaactcgactcacctcggcagggtg-acgcattgaagaagcgcgtcgag	144		
Qy	149	aattattagaacaattaaatacaaccagaagcgcacttatatacaaatgatgtttcaaacg	208		
Db	145	cctctcgcgaggaaactcggcgctttcatgcgcgcgcattgcgacgtgacgatctctcag	204		
Qy	209	atgaagaggttattaaatgggttttgagcaaatgtgttaaagatgttgccaatatgatgggtg	268		
Db	205	acga-----tcgaactcogtttttgcctcgtcgtggaacagcattgggcaagatcgacttcg	259		
Qy	269	tataatcattcaatcgcatatttgcgttaataatggaagacttaacgcgcgccttttctgaaactt	328		
Db	260	tcgtgcgcgcattgcgttctcgcacaaagacgagctgcgcggcgttatctcgcataacca	319		
Qy	329	cacgtgaaggcttctgttagctcaagaacattagttcttactcattaaacaattgtggctc	388		
Db	320	gcgcgcacactcaacccgcaccatggatattccgtgttctcgcgtgcgcgcgttgca	379		
Qy	389	atgaagcttaaaaaattaatgcgaaggtgttagcatgtttgcacaaacatatattaggtg	448		
Db	380	agcgcgcagaccatcatgaatgacgcggttcgatcatcacgcgttacctattacgcgcg	439		
Qy	449	gcgaattcgcagttcctcaaaattataatdgtatgggtgtgtctaagcgaagcgttagaagca	508		
Db	440	ccgaaaaaggtcatgccgaattacacacgtatggcgtggccaaaggcgcctcttgaagcca	499		
Qy	509	atgtataattattagcattagacttagtctgataataatcgcgttaatgcgaatttcag	568		
Db	500	gcgtgcgttatctcgcgcgtcgacctcggtaatcgcggcatccgcgtcaacgcgcgtttccg	559		
Qy	569	ctggtccaaatccgtacattaaagtcaaaaggtgtgggtgtttccaatacaaatctctaaag	628		
Db	560	ccggccgcgatcaagaacgtctgcggtctccggcatccgcgcgatttccgttacctgaagt	619		
Qy	629	aaatcgaagacgctgcaccttttaaaacgtaacgcttgatacaagtagaagtaggttaaacag	688		
Db	620	ggaacgaataaaatgcgcgcgtgaaagcgcaccttaccatcgaggaagtcgcgaactcg	679		
Qy	689	cggcttacttrttaagtgacttacaagtggcgttacaggtgaaaaatattcatcttagata	748		
Db	680	cgcctacctgttgcgaacctttcgaagccgtgcgcgcgtgcacccgtgaaatccaccatgtcgatt	739		
Qy	749	gcggattccacgcaat	764		
Db	740	ccgcgtatcacacat	755		

Search completed: September 22, 2002, 16:59:29  
Job time: 4310 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 22, 2002, 16:00:24 ; Search time 24.87 seconds  
(without alignments)  
251.425 Million cell updates/sec

Title: US-09-292-411A-2  
Perfect score: 1277  
Sequence: 1 MLNLENTYVINGTANKRSI.....LSSGVGTGENIHVDSGFRAIK 256

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA: \*  
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2: /cgn2.6/ptodata/2/1aa/5B\_COMB.pep:\*  
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4: /cgn2.6/ptodata/2/1aa/6B\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	542.5	42.5	262	1 US-08-241-766-9	Sequence 9, Appli
2	529.5	41.5	262	1 US-08-241-766-8	Sequence 8, Appli
3	322.5	25.3	390	4 US-09-586-719-2	Sequence 2, Appli
4	295.5	23.1	269	1 US-08-241-766-6	Sequence 6, Appli
5	292.5	22.9	269	1 US-08-241-766-7	Sequence 7, Appli
6	280.5	22.0	269	1 US-08-241-766-4	Sequence 4, Appli
7	278.5	21.8	269	1 US-08-241-766-5	Sequence 5, Appli
8	278.5	21.8	269	1 US-08-241-766-14	Sequence 14, Appli
9	190.5	14.9	262	4 US-09-363-189B-6	Sequence 6, Appli
10	179.5	14.1	292	3 US-09-109-205-2	Sequence 2, Appli
11	172	13.5	244	1 US-08-762-129-4	Sequence 4, Appli
12	171	13.4	244	1 US-08-762-129-3	Sequence 3, Appli
13	170	13.3	244	1 US-08-762-129-1	Sequence 1, Appli
14	169	13.2	295	3 US-09-002-298-5	Sequence 5, Appli
15	166	13.0	244	2 US-09-090-567-2	Sequence 2, Appli
16	165.5	13.0	255	4 US-08-815-225-4	Sequence 4, Appli
17	163	12.8	335	3 US-09-002-298-6	Sequence 6, Appli
18	157	12.3	335	3 US-09-109-205-19	Sequence 19, Appli
19	155.5	12.2	283	4 US-09-367-012-1	Sequence 1, Appli
20	153.5	12.0	303	3 US-09-002-298-1	Sequence 1, Appli
21	150	11.7	244	1 US-08-375-962B-13	Sequence 13, Appli
22	150	11.7	244	2 US-08-562-114B-13	Sequence 13, Appli
23	150	11.7	244	4 US-08-729-594A-13	Sequence 13, Appli
24	138	10.8	335	3 US-09-002-298-7	Sequence 7, Appli
25	131.5	10.3	256	1 US-08-594-808B-7	Sequence 7, Appli
26	126	9.9	246	3 US-09-238-481-2	Sequence 2, Appli
27	125.5	9.8	313	4 US-09-413-814-9	Sequence 9, Appli

28	124.5	9.7	231	2	US-08-336-198C-7	Sequence 7, Appli
29	123.5	9.7	261	4	US-09-468-738A-29	Sequence 29, Appli
30	121	9.5	243	4	US-09-239-052-2	Sequence 2, Appli
31	120.5	9.4	388	4	US-08-980-832-41	Sequence 41, Appli
32	120	9.4	246	6	5229279-7	Patent No. 5229279
33	119	9.3	333	1	US-08-440-856A-4	Sequence 4, Appli
34	112	8.8	247	1	US-08-241-766-13	Sequence 13, Appli
35	111	8.7	292	4	US-09-468-738A-2	Sequence 2, Appli
36	111	8.7	296	4	US-09-468-738A-23	Sequence 23, Appli
37	111	8.7	337	1	US-08-440-856A-3	Sequence 3, Appli
38	108	8.5	323	2	US-09-019-216-3	Sequence 3, Appli
39	106.5	8.3	315	3	US-08-793-035-9	Sequence 9, Appli
40	106.5	8.3	315	3	US-08-793-035-10	Sequence 10, Appli
41	106	8.3	186	4	US-08-858-207A-270	Sequence 270, App
42	105	8.2	252	3	US-08-822-322-8	Sequence 8, Appli
43	105	8.2	252	3	US-09-466-109-8	Sequence 8, Appli
44	104.5	8.2	257	4	US-09-287-097-2	Sequence 2, Appli
45	103.5	8.1	271	2	US-07-637-865-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-241-766-9  
; Sequence 9, Application US/08241766  
; Patent No. 5686590  
; GENERAL INFORMATION:  
; APPLICANT: JACOBS, W. R.  
; APPLICANT: COLLINS, D. M.  
; APPLICANT: BANERJEE, A.  
; APPLICANT: DELISLE, G. W.  
; APPLICANT: WILSON, T. M.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN INHA AGENT  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,766  
; FILING DATE: 12-MAY-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MONROY, GLADYS H.  
; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 25237-20003.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 262 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-241-766-9

Query Match 42.5% Score 542.5; DB 1; Length 262;  
Best Local Similarity 44.0%; Pred. No. 2.6e-46;  
Matches 110; Conservative 52; Mismatches 85; Indels 3; Gaps 2;



APPLICANT: DELISLE, G. W.  
 APPLICANT: WILSON, T. M.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
 TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN INHA AGENT  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/241,766  
 FILING DATE: 12-MAY-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MONROY, GLADYS H.  
 REGISTRATION NUMBER: 32,430  
 REFERENCE/DOCKET NUMBER: 25237-20003.20  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 269 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-241-766-6

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Query Match      23.1%; Score 295.5; DB 1; Length 269;
Best Local Similarity 34.1%; Pred. No. 1.2e-21;
Matches          91; Conservative 45; Mismatches 104; Indels 27; Gaps 9;

QY   4 LNKTYVMIGIANKRSTAFGVAKVVDLQGLAKLVITYRKSRKKELEKLLEQLNOPEAHLY 63
    || :||| |||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db   5 LEGRRIIVTGIITSSIAFHIAKVAQEAGAEVLVTGDR--LKLVKRIADRLPKP-APLL 61

QY   64 QIDVQSDEEVINGEQIQTGVQ---NIDGYHSTAFANMEDLR-CRRSETSRSGFLLAQD 119
    :||||:| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db   62 ELDVQNEEHLSTLADRITAETEGENKDGVVHSICFMPSQGGMIPPFDAPEYDVSRGIH 121

QY   120 ISSYSLATVAHEAKKLMPGGSGSIATTYLGGEF---AVQNYVMGVAKASLEANVKYLA 175
    ||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db   122 ISAYSIASLAKAVLPINWPGGGIY-----GMDFPTTRAMPAYNNMTVAKSALSVNRFA 176

QY   176 LDLGPDMIRNAISAGPIRTLSAKG-VGG-----FNTILKEIBERAPLKNRV-DQV 224
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db   177 REACKVGVRSNLVAAGPIRTLANSATVGGALGDGAQQMQLLEEGWDORAPLGNMKDPT 236

QY   225 EVGKTAAYLLSDISSGVGTGENIHVDSG 251

Db   237 PVAKTVCALLSDWLPAATTGTGVYADGG 263
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RESULT 5  
US-08-241-766-7  
; Sequence 7, Application US/08241766  
; Patent No. 5686590  
; GENERAL INFORMATION:  
; APPLICANT: JACOBS, W. R.  
; APPLICANT: COLLINS, D. M.  
; APPLICANT: BANERJEE, A.  
; APPLICANT: DELISLE, G. W.  
; APPLICANT: WILSON, T. M.

```

: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
:
: TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN inhA AGENT
:
: NUMBER OF SEQUENCES: 14
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: MORRISON & FOERSTER
:
: STREET: 755 Page Mill Road
:
: CITY: Palo Alto
:
: STATE: CA
:
: COUNTRY: USA
:
: ZIP: 94304-1018
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: Patent In Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/241,766
:
: FILING DATE: 12-MAY-1994
:
: CLASSIFICATION: 514
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: MONROY, GLADYS H.
:
: REGISTRATION NUMBER: 32,430
:
: REFERENCE/DOCKET NUMBER: 25237-20003.20
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (415) 813-5600
:
: TELEFAX: (415) 494-0792
:
: TELEX: 706141
:
: INFORMATION FOR SEQ ID NO: 7:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 269 amino acids
:
: TYPE: amino acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: US-08-241-766-7

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Query Match	22.9%	Score	292.5;	DB 1;	Length	269;																																																		
Best Local Similarity	33.7%;	Pred. No.	2.3e-21;																																																					
Matches	90;	Conservative	46;	Mismatches	104;	Indels	27;	Gaps	9;																																															
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QY	64	Q	I	D	V	Q	S	D	E	E	V	I	N	G	T	G	K	V	G	--	N	D	V	G	H	S	T	A	F	A	N	M	E	D	L	R	--	G	R	S	E	S	R	E	G	F	L	L	A	Q	119					
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QY	120	I	S	S	Y	S	L	I	V	A	H	E	A	K	L	M	P	E	G	S	I	V	A	T	T	V	L	G	G	E	F	---	A	V	Q	N	Y	N	Y	G	V	A	K	A	S	E	A	N	K	Y	L	A	175			
Db	122	I	S	A	Y	S	A	S	L	A	K	A	V	L	P	I	N	N	P	G	G	I	V	---	G	M	D	F	O	T	T	R	A	M	P	A	Y	N	N	W	T	V	A	K	S	A	L	E	S	V	N	R	F	V	A	176
QY	176	L	D	L	G	P	D	N	R	I	N	A	I	S	A	G	P	I	R	T	L	S	A	K	--	Y	G	G	-----	F	N	T	I	L	E	I	E	I	E	R	A	K	E	R	N	--	Q	D	V	224						
Db	177	R	E	A	C	K	V	G	R	S	N	L	V	A	A	G	P	I	R	T	L	A	M	S	A	I	V	G	G	A	L	G	D	E	A	G	Q	M	L	E	S	G	W	O	R	A	P	L	G	N	M	K	D	P	T	236
QY	225	E	V	G	T	A	A	Y	L	L	S	D	L	S	S	G	V	T	G	E	N	I	H	V	D	S	G	251																												
Db	237	P	V	A	K	T	V	C	A	L	L	S	D	M	L	P	A	T	T	G	T	T	V	I	A	D	G	263																												

RESULT 6  
US-08-241-766-4  
; Sequence 4, Application US/08241766  
; Patent No. 5686590  
; GENERAL INFORMATION:  
; APPLICANT: JACOBS, W. R.  
; APPLICANT: COLLINS, D. W.  
; APPLICANT: BANERJEE, A.  
; APPLICANT: GELISJE, G. W.  
; APPLICANT: WILSON, T. M.  
; TITLE OF INVENTION: METHODS AND  
; TITLE OF INVENTION: TREATING

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; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 12-MAY-1994  
; APPLICATION NUMBER: US/08/241,766  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MONROY, GLADYS H.  
; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 25237-20003.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 269 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-241-766-14

Query Match 21.8%; Score 278.5; DB 1; Length 269;  
Best Local Similarity 31.4%; Pred. No. 5.8e-20;  
Matches 86; Conservative 57; Mismatches 94; Indels 37; Gaps 11;  
QY 4 LENKTVIMGINKRSTAFQVAKVLDQLGAKLVFTYRKRSRKELEKLEQLNQPEAHLY 63  
Db 5 LDGKRILVSGIITDSIAHIAHVAQEQAGLVLT-GFDELRL-IQRTDRL-PAPAPLL 61  
QY 64 QIDVQDEEVINGFEIQKDVG---NIDGYHSHAFANMEDL-----RGFSETSRGFF 114  
Db 62 ELDVQNEEHLASLAGRVAIGAGNKLGVVHAIGFMPQTMGMPFADAPYADVSK--- 118  
QY 115 LLAQDISSYSLTVAHEAKKLMPGEGSIVATTYLGGEF---AVQYNYMGVAKASLEA 170  
Db 119 --GIHSAYSASYAMAKALLPIMPGGISV-----GMDFPSRAMPAYNNMTVAKSALES 171  
QY 171 VKYALDLGPDNIRVNAISAGPIRTLSAKGV-----GGFNTILKE-IEERAPLKN 220  
Db 172 NRVAREAGKYGVRSNLVRAAGPIRTLSAIVGALGEEAGAGIQLLEEGWDQRAPIGWN 231  
QY 221 V-DOVEVGKTAAYLLSDLSGGVTGENIHVDSPGH 253  
Db 232 MKDATPVAKTVCALLSDWLPATTTGDIYADGGAH 265

RESULT 9  
US-09-363-1898-6  
; Sequence 6, Application US/093631898  
; Patent No. 6242228  
; GENERAL INFORMATION:  
; APPLICANT: SUGIYAMA, MASAKAZU  
; APPLICANT: TONOUCHI, NAOTO  
; APPLICANT: SUZUKI, SHUNICHI  
; APPLICANT: YOKOZAKI, KENZO  
; TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF  
; FILE REFERENCE: 0010-1024-0  
; CURRENT APPLICATION NUMBER: US/09/363,189B  
; CURRENT FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: JP10-216047  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6

; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Gluconobacter oxydans  
; US-09-363-1898-6  
Query Match 14.9%; Score 190.5; DB 4; Length 262;  
Best Local Similarity 29.6%; Pred. No. 3.4e-11;  
Matches 68; Conservative 41; Mismatches 96; Indels 25; Gaps 7;  
QY 42 ERSRKELEKLEQLNOP--EAHLYQIDVQDEEVINGFEIQKDVGNIDGVYHSI-----A 95  
Db 38 DMNREALEAKAEASVREKGVARSYVCDVTSEEAVIGTVDSVVRDFGKIDFLFNAGYQGA 97  
QY 96 FANMEDLRGRFSETSRGFFLLAQDISSYSLTVAHEAKKLMPGEGSIVATTYLGGEFAVQ 155  
Db 98 FAPVQDYP--DDFAR---VLTINVTGAFHVLKAVSRQMITQNYGRIVNTASMAVKGPP 152  
QY 156 NYNMGVAKASLEANVKYLAIDLGPDIRVNAISAGPIR-----TLSAK-GVGGFN 205  
Db 153 NMAAYGASKGAIILTAALDLAPYINRVNAISPGYMGPGFMWROVLOAKVGSQYFS 212  
QY 206 TILKEIER-----APLKRNVDOVEVGKTAAYLLSDLSGGVTGENIHVDSPG 251  
Db 213 TDPKVVAQMGISVPMPHRYGDINEIPGVVAFLLGDDSSFTGYNLPAGG 262

RESULT 10  
US-09-109-205-2  
; Sequence 2, Application US/09109205  
; Patent No. 6057140  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Gorgone, Gina  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Baughn, Mariah R.  
; APPLICANT: Yue, Henry  
; TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/109,205  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cerrone, Michael C.  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0542 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-855-0572  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 292 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

IMMEDIATE SOURCE:  
LIBRARY: PROSTUT12  
CLONE: 1810320  
US-09-109-205-2

Query Match 14.1%; Score 179.5; DB 3; Length 292;  
Best Local Similarity 29.3%; Pred. No. 5e-10;  
Matches 76; Conservative 42; Mismatches 116; Indels 25; Gaps 11;  
QY 4 LENKTVVINGIANKRSIAFGVAKVLDOLGAKLVFTYRK-ERSRKELEKLEQLNQPBAHL 62  
DB 26 LDKVAFITG--GGSGIGFRIAEIFMRHGCHTVIASRSLPRLVLTAAKLAGATGRCLPL 83  
QY 63 YQIDVQSDDEVINGFEQIGKDVGNIDGVVHSIAFANMEDLRGF-----SETSRGFFLLAQ 118  
DB 84 -SMDVRAPPVNAVDQALKEFRIDILNCAA-----GNFLCPAGALSFNFAKTVM 134  
QY 119 DI---SSYSLTIVAHEAKLMPEGGSIV-ATTYLGGE-FAVONYNVMGVAKASLEANYKY 173  
DB 135 DIDTSGTFNVSRVLYE-KFFRDHGGVIVNITATLGNRQALQVH--AGSAAVAVDAMTRH 191  
QY 174 LALDGPONIRNVAISAGPIR-TLSAKGVGGFNTILKELEERAPLKRNVDOVEVGKTAAY 232  
DB 192 LAVENGPNIRNVAISAGPIRSGTGLRRLLGGPQASLSTKVTASPLRLGNKTEIAHSVLY 251  
QY 233 LLSLSSGVTGENIRHDSG 251  
DB 252 LASPLASYVTGAVLVADGG 270

RESULT 11  
US-08-762-129-4  
Sequence 4, Application US/08762129  
Patent No. 5756299  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: A NOVEL HUMAN CARBONYL REDUCTASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/762,129  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0171 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 50004  
US-08-762-129-4

Query Match 13.5%; Score 172; DB 1; Length 244;  
Best Local Similarity 24.5%; Pred. No. 2.1e-09;  
Matches 63; Conservative 53; Mismatches 121; Indels 20; Gaps 7;  
QY 2 LNLENKTVVINGIANKRSIAFGVAKVLDOLGAKLVFTYRKERSRKELEKLEQLNQPBAH 61  
DB 3 LNFSGRLALVTGAG--KGIGRDTVKALHASGAKVYAV---TRTNSDLVSLAKECPGIEPV 57  
QY 62 LYQI-DVQSDDEVINGFEQIGKDVGNIDGVVHSIAFANMEDLRGFSETSRGFFLLAODI 120  
DB 58 CVDIGDWDATKALGG-----IGVDLLVNNAALVIMQP-----FLEVTREAFDRSPSV 106  
QY 121 SSYSLTIYAH-EAKLMPEG--GSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALD 177  
DB 107 NLRSVFQSQVMARDMINRGVPGSIVNVYSSMVAHVTFEPNLITYSSTKGAMTMTKAMAME 166  
QY 178 LQPDNIRNVAISAGPIRPLSAKVGCGFNTILKELEERAPLKRNVDOVEVGKTAAYLLSD 237  
DB 167 LGPHKIRVNSVNTYVLLTDMGKVSADPEFARKLKERHPLRKAFAEVEDVNSILFLSDR 226  
QY 238 SSGVTGENIRHDSGPHA 254  
DB 227 SASSTGGGILVDAGYLA 243

RESULT 12  
US-08-762-129-3  
Sequence 3, Application US/08762129  
Patent No. 5756299  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: A NOVEL HUMAN CARBONYL REDUCTASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/762,129  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0171 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear



IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 416425  
US-08-762-129-3

Query Match 13.4%; Score 171; DB 1; Length 244;  
Best Local Similarity 24.1%; Pred. No. 2.7e-09;  
Matches 58; Conservative 57; Mismatches 108; Indels 18; Gaps 6;  
QY 18 RSTAFGAKVLDQGLAKLVFTYRKRSRKELEKLLQNOPEAHLYQI-DVQSDVEEVING 76  
DB 17 KGIGRTVRLVHSGARVAV---TFTNGDLVSLSQECPIEPVCVDLGDWEATERALGG 73  
QY 77 FEOIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGREGFLLAQDISYSITIVAH-EAKKL 135  
DB 74 -----VGPVDLLVNNAAVALMQP---FLDPTKEVDFORSFNVLRSVFQVSOIVARSM 122  
QY 136 MPFG--GSIVATYTLGGEFAVQNYVMGVAKASLEANKVYLALDLPDNIIRVNAISAGPI 193  
DB 123 IERGVPGSIVNVSMSYSHVTPYGLAAYSTKGAMTMTKSMAMELGPCHKIRVNSVNPVTV 182  
QY 194 RTLSAKGVGFGFTILKEIERAPLKRNVQVEVGKTAAYLLSDLSGGVTGENIHVDSGFH 253  
DB 183 LTAMGRSVTSDPELARKLKERHPMKFAEVEDVNSILFLSDRSASTSGSSIFVDAGYL 242  
QY 254 A 254  
DB 243 A 243

RESULT 13  
US-08-762-129-1  
Sequence 1, Application US/08762129  
Patent No. 5756299  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: A NOVEL HUMAN CARBONYL REDUCTASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/762,129  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0171 US  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

IMMEDIATE SOURCE:  
LIBRARY: Consensus  
CLONE: Consensus  
US-08-762-129-1

Query Match 13.3%; Score 170; DB 1; Length 244;  
Best Local Similarity 24.9%; Pred. No. 3.4e-09;  
Matches 64; Conservative 53; Mismatches 120; Indels 20; Gaps 7;  
QY 2 LNLNKTYVIMGTIANRSTAFGVAKVLDQGLAKLVFTYRKRSRKELEKLLQNOPEAH 61  
DB 3 LFTAGRLVLTGAG--KGIGRTVQALHATGARVAV---SRTQADLDSLVRPCPGIEPV 57  
QY 62 LYQI-DVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGREGFLLAQDI 120  
DB 58 CVDLGDWEATERALG-----SVGPVDLLVNNAAVALMQP---FLEVTKFAFDRSFV 106  
QY 121 SSVSLTIVAH-EAKKLMPG--CSIIVATYTLGGEFAVQNYVMGVAKASLEANKVYLALD 177  
DB 107 NLRVAVTQVSOIVARGLIARGVPGAIIVNVSSQCSQRAVTNHSVYCSKTKGALDMLTKVNALE 166  
QY 178 LGPDNIIRVNAISAGPIRTLSAKGVGFGFTILKEIERAPLKRNVQVEVGKTAAYLLSDL 237  
DB 167 LGPHKIRVNAVNTVVTWTSMGQATWSDPHKAKTXNRIPIXGKFAEVEHHVNNAILFLLSDR 226  
QY 238 SSGVTGENIHVDSGFHA 254  
DB 227 SGMTTGSTLPVEGGFWA 243

RESULT 14  
US-09-002-298-5  
Sequence 5, Application US/09002298  
Patent No. 6046001  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
APPLICANT: Tang, Y. Tom  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: HUMAN FATTY ACID BETA-OXIDATION ENZYMES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/002,298  
FILING DATE: Filed Herewith  
PRIOR APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0453 US  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 295 amino acids  
TYPE: amino acid



```

Query Match      100.0%; Score 1277; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 M L N L E N K T V I M G I A N K R S I A F G V A K L V D Q L G A K L V F Y R K R S R K E L K L L B Q L N O P E A 60
  |||||
1 M L N L E N K T V I M G I A N K R S I A F G V A K L V D Q L G A K L V F Y R K R S R K E L K L L B Q L N O P E A 60
  |||||

```

QY 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSAFANMEDLRGRFSETSGREGFLLAQDI 120  
Db 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSAFANMEDLRGRFSETSGREGFLLAQDI 120  
QY 121 SSYSLTIWAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALDLGP 180  
Db 121 SSYSLTIWAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALDLGP 180  
QY 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
Db 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
QY 241 VTGENIHVDSGFHAIK 256  
Db 241 VTGENIHVDSGFHAIK 256

RESULT 2  
PCT-US02-03987-5228  
; Sequence 5228, Application PC/TUS0203987  
; GENERAL INFORMATION:  
; APPLICANT: Elittra Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits  
; FILE REFERENCE: ELITRA.028VPC  
; CURRENT APPLICATION NUMBER: PCT/US02/03987  
; CURRENT FILING DATE: 2002-02-02  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 15811  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5228  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
PCT-US02-03987-5228

Query Match 100.0%; Score 1277; DB 1; Length 256;  
Best Local Similarity 100.0%; Pred. No. 8.4e-118;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQGLAKLVFTYRKERSRKELEKLEQLNOPEA 60  
Db 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQGLAKLVFTYRKERSRKELEKLEQLNOPEA 60  
QY 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSAFANMEDLRGRFSETSGREGFLLAQDI 120  
Db 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSAFANMEDLRGRFSETSGREGFLLAQDI 120  
QY 121 SSYSLTIWAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALDLGP 180  
Db 121 SSYSLTIWAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALDLGP 180  
QY 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
Db 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
QY 241 VTGENIHVDSGFHAIK 256  
Db 241 VTGENIHVDSGFHAIK 256

RESULT 3  
PCT-US02-03987-12535  
; Sequence 12535, Application PC/TUS0203987  
; GENERAL INFORMATION:  
; APPLICANT: Elittra Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits  
; FILE REFERENCE: ELITRA.028VPC  
; CURRENT APPLICATION NUMBER: PCT/US02/03987  
; CURRENT FILING DATE: 2002-02-02

; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 15811  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 12535  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
PCT-US02-03987-12535

Query Match 100.0%; Score 1277; DB 1; Length 256;  
Best Local Similarity 100.0%; Pred. No. 8.4e-118;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQGLAKLVFTYRKERSRKELEKLEQLNOPEA 60  
Db 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQGLAKLVFTYRKERSRKELEKLEQLNOPEA 60  
QY 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSAFANMEDLRGRFSETSGREGFLLAQDI 120  
Db 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSAFANMEDLRGRFSETSGREGFLLAQDI 120  
QY 121 SSYSLTIWAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALDLGP 180  
Db 121 SSYSLTIWAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALDLGP 180  
QY 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
Db 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
QY 241 VTGENIHVDSGFHAIK 256  
Db 241 VTGENIHVDSGFHAIK 256

RESULT 4  
PCT-US02-03987-12892  
; Sequence 12892, Application PC/TUS0203987  
; GENERAL INFORMATION:  
; APPLICANT: Elittra Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits  
; FILE REFERENCE: ELITRA.028VPC  
; CURRENT APPLICATION NUMBER: PCT/US02/03987  
; CURRENT FILING DATE: 2002-02-02  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 15811  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 12892  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
PCT-US02-03987-12892

Query Match 100.0%; Score 1277; DB 1; Length 256;  
Best Local Similarity 100.0%; Pred. No. 8.4e-118;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQGLAKLVFTYRKERSRKELEKLEQLNOPEA 60  
Db 1 MLNLENKTYVIMGTANKRSIAFGVAKVLDQGLAKLVFTYRKERSRKELEKLEQLNOPEA 60  
QY 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSAFANMEDLRGRFSETSGREGFLLAQDI 120  
Db 61 HLYQIDVQSDDEVINGFEQIGKDVGNIDGVYHSAFANMEDLRGRFSETSGREGFLLAQDI 120  
QY 121 SSYSLTIWAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALDLGP 180  
Db 121 SSYSLTIWAHEAKKLMPGGGSIVATTYLGGEFAVQNYNVMGVAKASLEANYKYLALDLGP 180

QY 181 DNIIRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240  
Db 181 DNIIRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240  
QY 241 VTGENIHVDGSGFHAIK 256  
Db 241 VTGENIHVDGSGFHAIK 256

RESULT 5  
US-08-790-043-1  
; Sequence 1, Application US/08790043  
; GENERAL INFORMATION:  
; APPLICANT: Lonsdale, John  
; APPLICANT: Milner, Peter  
; APPLICANT: Payne, David  
; APPLICANT: Pearson, Stewart  
; TITLE OF INVENTION: Novel Fabi  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/790,043  
; FILING DATE: 24-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/024845  
; FILING DATE: 28-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gimmi, Edward R  
; REGISTRATION NUMBER: 38,891  
; REFERENCE/DOCKET NUMBER: GM50005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-4478  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-790-043-1

Query Match 100.0%; Score 1277; DB 11; Length 256;  
Best Local Similarity 100.0%; Pred. No. 8.4e-118;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLNLENKTVYIMGIANKRSIAFGVAKVLDOLGAKLVFTYRKERSRKELEKLLQLNQPEA 60  
Db 1 MLNLENKTVYIMGIANKRSIAFGVAKVLDOLGAKLVFTYRKERSRKELEKLLQLNQPEA 60  
QY 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGYHSIAFANMEDLGRFSETSRGFFLLAQDI 120  
Db 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGYHSIAFANMEDLGRFSETSRGFFLLAQDI 120  
QY 121 SSVSLTIVAEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180  
Db 121 SSVSLTIVAEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180  
QY 181 DNIIRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240

Db 181 DNIIRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240  
QY 241 VTGENIHVDGSGFHAIK 256  
Db 241 VTGENIHVDGSGFHAIK 256  
RESULT 6  
US-08-790-043A-1  
; Sequence 1, Application US/08790043A  
; GENERAL INFORMATION:  
; APPLICANT: Lonsdale, John  
; APPLICANT: Milner, Peter  
; APPLICANT: Payne, David  
; APPLICANT: Pearson, Stewart  
; TITLE OF INVENTION: Novel Fabi  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/790,043A  
; FILING DATE: 28-August-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/024845  
; FILING DATE: 28-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gimmi, Edward R  
; REGISTRATION NUMBER: 38,891  
; REFERENCE/DOCKET NUMBER: GM50005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-4478  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-790-043A-1

Query Match 100.0%; Score 1277; DB 11; Length 256;  
Best Local Similarity 100.0%; Pred. No. 8.4e-118;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLNLENKTVYIMGIANKRSIAFGVAKVLDOLGAKLVFTYRKERSRKELEKLLQLNQPEA 60  
Db 1 MLNLENKTVYIMGIANKRSIAFGVAKVLDOLGAKLVFTYRKERSRKELEKLLQLNQPEA 60  
QY 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGYHSIAFANMEDLGRFSETSRGFFLLAQDI 120  
Db 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGYHSIAFANMEDLGRFSETSRGFFLLAQDI 120  
QY 121 SSVSLTIVAEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180  
Db 121 SSVSLTIVAEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180  
QY 181 DNIIRVNAISAGPIRTLSAKGVGGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDSSG 240

Db	181	DNTRVNAISAGPTITLSAKGVGGENTILKEIEERAPLKRNVQDVGVGKTAAYLLSDLSG	240
Qy	241	VTGENIHVDGSPFAIK	256
Db	241	VTGENIHVDGSPFAIK	256

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RESULT 7
US-08-790-043B-2
; Sequence 2, Application US/08790043B
; GENERAL INFORMATION:
;
; APPLICANT: Payne, David
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Pearson, Stewart
;
; TITLE OF INVENTION: F I
; NUMBER OF SEQUENCES: 2
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790_043B

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Query Match	100.0%	Score 1277;	DB 11;	Length 256;
Best Local Similarity	100.0%;	Pred. No. 8.4e-110;		
Matches 256;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	M L N L K N T Y V I M G I A N K S I A F G V A K V L D Q L G A K L V F T Y K R S R K E L K L L E Q L N Q P E A	60	
DB	1	M L N L K N T Y V I M G I A N K S I A F G V A K V L D Q L G A K L V F T Y K R S R K E L K L L E Q L N Q P E A	60	
QY	61	H Y I Q I D V O S D E V I N F F Q I O K D V G N I D G V Y H S T A F A N M E D L G R F S E T S S R G F L L A Q D I	120	
DB	61	H Y I Q I D V O S D E V I N F F Q I O K D V G N I D G V Y H S T A F A N M E D L G R F S E T S S R G F L L A Q D I	120	
QY	121	S S Y S L T I V A H E A K L M P E G G S I V A T T Y L G G E F A V Q N Y N V G V A K A S L E A N V K Y L A L D L G P	180	
DB	121	S S Y S L T I V A H E A K L M P E G G S I V A T T Y L G G E F A V Q N Y N V G V A K A S L E A N V K Y L A L D L G P	180	
QY	181	D N I R N Y A L S A G P I R T L S A K G V G G F N T I L K E I E R A P L K R N V D O V E G K T A A Y L L S D L S S G	240	
DB	181	D N I R N Y A L S A G P I R T L S A K G V G G F N T I L K E I E R A P L K R N V D O V E G K T A A Y L L S D L S S G	240	

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Qy      241 VTGENIHVDSGFHAIK 256
        |||||
Db      241 VTGENIHVDSGFHAIK 256

RESULT      8
US-09-292-411-2
: Sequence 2, Application US/09292411
: GENERAL INFORMATION:
:
: APPLICANT: Payne, David
: APPLICANT: Lonsdale, John
: APPLICANT: Milner, Peter
: APPLICANT: Pearson, Stewart
: TITLE OF INVENTION: FAB I
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dechert Price & Rhoads
: STREET: 4000 Bell Atlantic Tower, 1717 Arch Street
: CITY: Philadelphia
: STATE: PA
: COUNTRY: US
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/292,411
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/790,043
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Falk, Stephen T
: REGISTRATION NUMBER: 36,795
: REFERENCE/DOCKET NUMBER: GM50005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-994-2488
: TELEFAX: 215-994-2222
: TELEX:
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 256 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-292-411-2

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Query Match	100.0%;	Score 1277;	DB 16;	Length 256;
Best Local Similarity	100.0%;	Pred. No. 8.4e-118;		
Matches 256;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MLNLNENKTYVMGTANKRSTAFGVAKYVDQLGAKLVFTYRKRSRKEKEKLEQLNQPEA	60	
Db	1	MLNLNENKTYVMGTANKRSTAFGVAKYVDQLGAKLVFTYRKRSRKEKEKLEQLNQPEA	60	
Qy	61	HLVQIDVQSDBEVINGFEQIGKDVGNIDGVYHSTAFANMEDLRGRFSETSGREGFLAQDI	120	
Db	61	HLVQIDVQSDBEVINGFEQIGKDVGNIDGVYHSTAFANMEDLRGRFSETSGREGFLAQDI	120	
Qy	121	SSYSLTTVAHEAKKLMPGGSGIVATTYLGGBFVQNVNMGVAKASLEANYKYIALDLGP	180	
Db	121	SSYSLTTVAHEAKKLMPGGSGIVATTYLGGBFVQNVNMGVAKASLEANYKYIALDLGP	180	
Qy	181	DNTRVNIAISAGPIRTLAKGVGGGNTILKETEERAPLKRNVDDQVEVGKTAAYLLSDSSG	240	
Db	181	DNTRVNIAISAGPIRTLAKGVGGGNTILKETEERAPLKRNVDDQVEVGKTAAYLLSDSSG	240	
Qy	241	VTGENIHVDSGFHAK 256		

```
Db 241 VTGENIHVDSGFHAIK 256
;
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/292,412
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/790,043
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM50005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-292-412-2
;
; Query Match 100.0%; Score 1277; DB 16; Length 256;
; Best Local Similarity 100.0%; Pred. No. 8.4e-118;
; Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 MLNLEKTVVINGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLQNLQPEA 60
; DB 1 MLNLEKTVVINGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLQNLQPEA 60
;
; QY 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANWEDLGRFSETSRGFLLAQDI 120
; DB 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANWEDLGRFSETSRGFLLAQDI 120
;
; QY 121 SSVSLTIVAHKAKLMPEGGSIVATTYLGGEFAVQNYNVGVAKASLEANVKYLAIDLGP 180
; DB 121 SSVSLTIVAHKAKLMPEGGSIVATTYLGGEFAVQNYNVGVAKASLEANVKYLAIDLGP 180
;
; QY 181 DNIRVNAISAGPRTLSAKGVGFNTILKEIERAPLKRNVQDQVEVGKTAAYLLSLSSG 240
; DB 181 DNIRVNAISAGPRTLSAKGVGFNTILKEIERAPLKRNVQDQVEVGKTAAYLLSLSSG 240
;
; QY 241 VTGENIHVDSGFHAIK 256
; DB 241 VTGENIHVDSGFHAIK 256
;
; RESULT 11
; US-09-815-242-5228
; Sequence 5228, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
;
;
; Db 241 VTGENIHVDSGFHAIK 256
;
; Query Match 100.0%; Score 1277; DB 16; Length 256;
; Best Local Similarity 100.0%; Pred. No. 8.4e-118;
; Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 MLNLEKTVVINGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLQNLQPEA 60
; DB 1 MLNLEKTVVINGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLQNLQPEA 60
;
; QY 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANWEDLGRFSETSRGFLLAQDI 120
; DB 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANWEDLGRFSETSRGFLLAQDI 120
;
; QY 121 SSVSLTIVAHKAKLMPEGGSIVATTYLGGEFAVQNYNVGVAKASLEANVKYLAIDLGP 180
; DB 121 SSVSLTIVAHKAKLMPEGGSIVATTYLGGEFAVQNYNVGVAKASLEANVKYLAIDLGP 180
;
; QY 181 DNIRVNAISAGPRTLSAKGVGFNTILKEIERAPLKRNVQDQVEVGKTAAYLLSLSSG 240
; DB 181 DNIRVNAISAGPRTLSAKGVGFNTILKEIERAPLKRNVQDQVEVGKTAAYLLSLSSG 240
;
; QY 241 VTGENIHVDSGFHAIK 256
; DB 241 VTGENIHVDSGFHAIK 256
;
; RESULT 10
; US-09-292-412-2
; Sequence 2, Application US/09292412
; GENERAL INFORMATION:
; APPLICANT: Payne, David
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: FAB I
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
;
; Db 241 VTGENIHVDSGFHAIK 256
;
; Query Match 100.0%; Score 1277; DB 16; Length 256;
; Best Local Similarity 100.0%; Pred. No. 8.4e-118;
; Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 MLNLEKTVVINGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLQNLQPEA 60
; DB 1 MLNLEKTVVINGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLQNLQPEA 60
;
; QY 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANWEDLGRFSETSRGFLLAQDI 120
; DB 61 HLYQIDVQSDDEEVINGFEQIGKDVGNIDGVYHSIAFANWEDLGRFSETSRGFLLAQDI 120
;
; QY 121 SSVSLTIVAHKAKLMPEGGSIVATTYLGGEFAVQNYNVGVAKASLEANVKYLAIDLGP 180
; DB 121 SSVSLTIVAHKAKLMPEGGSIVATTYLGGEFAVQNYNVGVAKASLEANVKYLAIDLGP 180
;
; QY 181 DNIRVNAISAGPRTLSAKGVGFNTILKEIERAPLKRNVQDQVEVGKTAAYLLSLSSG 240
; DB 181 DNIRVNAISAGPRTLSAKGVGFNTILKEIERAPLKRNVQDQVEVGKTAAYLLSLSSG 240
;
; QY 241 VTGENIHVDSGFHAIK 256
; DB 241 VTGENIHVDSGFHAIK 256
;
; RESULT 9
; US-09-292-411a-2
; Sequence 2, Application US/09292411a
; GENERAL INFORMATION:
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: Fabi
; FILE REFERENCE: GM50005-D1
; CURRENT APPLICATION NUMBER: US/09/292,411a
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 08/790,043
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: US 60/024,845
; PRIOR FILING DATE: 1996-08-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
; US-09-292-411a-2
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; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5228  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-5228

Query Match 100.0%; Score 1277; DB 22; Length 256;  
Best Local Similarity 100.0%; Pred. No. 8.4e-118;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNLENKTYIVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSKELEKLEQLNQPEA 60  
Db 1 MNLENKTYIVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSKELEKLEQLNQPEA 60  
  
QY 61 HLYQIDVQSDVEEVINGFQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLAADI 120  
Db 61 HLYQIDVQSDVEEVINGFQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLAADI 120  
  
QY 121 SSYSLTIVAHAKKLMPEGGISIVATTYLGGEFAVONYNMVGAKASLEANYKYIALDLGP 180  
Db 121 SSYSLTIVAHAKKLMPEGGISIVATTYLGGEFAVONYNMVGAKASLEANYKYIALDLGP 180  
  
QY 181 DNIRVNASAGPIRTLSAKGVGGNTILKETEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
Db 181 DNIRVNASAGPIRTLSAKGVGGNTILKETEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
  
QY 241 VTGENIHVDSGFHAIK 256  
Db 241 VTGENIHVDSGFHAIK 256

RESULT 12  
US-09-815-242-12535  
; Sequence 12535, Application US/09815242  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011a  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12535  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-12535

Query Match 100.0%; Score 1277; DB 22; Length 256;  
Best Local Similarity 100.0%; Pred. No. 8.4e-118;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNLENKTYIVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSKELEKLEQLNQPEA 60  
Db 1 MNLENKTYIVIMGTANKRSIAFGVAKVLDQLGAKLVFTYRKERSKELEKLEQLNQPEA 60  
  
QY 61 HLYQIDVQSDVEEVINGFQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLAADI 120  
Db 61 HLYQIDVQSDVEEVINGFQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLAADI 120  
  
QY 121 SSYSLTIVAHAKKLMPEGGISIVATTYLGGEFAVONYNMVGAKASLEANYKYIALDLGP 180  
Db 121 SSYSLTIVAHAKKLMPEGGISIVATTYLGGEFAVONYNMVGAKASLEANYKYIALDLGP 180  
  
QY 181 DNIRVNASAGPIRTLSAKGVGGNTILKETEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
Db 181 DNIRVNASAGPIRTLSAKGVGGNTILKETEERAPLKRNVDOVEVGKTAAYLLSDLSG 240  
  
QY 241 VTGENIHVDSGFHAIK 256  
Db 241 VTGENIHVDSGFHAIK 256

RESULT 13  
US-09-815-242-12892  
; Sequence 12892, Application US/09815242  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011a  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12892  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-12892



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Query Match      100.0%; Score 1277; DB 22; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFFLLAQDI 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFFLLAQDI 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 DNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSG 240
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 DNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSG 240
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 241 VTGENIHVDSGFHAIK 256
   ||||||||||||||||||
Db 241 VTGENIHVDSGFHAIK 256
   ||||||||||||||||||

RESULT 14
US-10-009-219-2
; Sequence 2, Application US/10009219
; GENERAL INFORMATION:
; APPLICANT: DEWOLF, WALTER E.
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS
; FILE REFERENCE: GMS00056
; CURRENT APPLICATION NUMBER: US/10/009,219
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PCT/US00/12104
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-009-219-2

Query Match      100.0%; Score 1277; DB 24; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFFLLAQDI 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFFLLAQDI 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 DNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSG 240
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 DNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSG 240
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 241 VTGENIHVDSGFHAIK 256
   ||||||||||||||||||
Db 241 VTGENIHVDSGFHAIK 256
   ||||||||||||||||||
```

```
RESULT 15
US-10-072-851-5228
; Sequence 5228, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,851
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5228
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-072-851-5228
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Query Match      100.0%; Score 1277; DB 24; Length 256;
Best Local Similarity 100.0%; Pred. No. 8.4e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MLNLENTVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLLEQLNOPEA 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFFLLAQDI 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSRGFFLLAQDI 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 SSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNMGVAKASLEANVKYLAIDLGP 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 DNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSG 240
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 DNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVDOVEVGKTAAYLLSDLSG 240
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 241 VTGENIHVDSGFHAIK 256
   ||||||||||||||||||
Db 241 VTGENIHVDSGFHAIK 256
   ||||||||||||||||||
```

Search completed: September 22, 2002, 17:03:32  
Job time: 3453 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 22, 2002, 16:07:04 ; Search time 100.11 Seconds  
(without alignments)  
684.068 Million cell updates/sec

Title: US-09-292-411A-2  
Perfect score: 1277  
Sequence: 1 MLNLENTYVIMGIANKRSI.....LSSGVGTGENIHVDSGFHAIK 256

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 947138 seqs, 267508082 residues

Total number of hits satisfying chosen parameters: 947138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_AA\_New.\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	256	5	US-09-791-537-111094
2	1263	98.9	255	6	US-10-089-019-12
3	1156	90.5	256	6	US-10-138-701-6
4	796	62.3	259	7	US-60-360-039-16488
5	767	60.1	260	7	US-60-360-039-17364
6	749	58.7	258	5	US-09-791-537-130900
7	749	58.7	269	5	US-09-791-537-2330
8	749	58.7	269	7	US-60-360-039-17696
9	626.5	49.1	260	7	US-60-360-039-20054
10	624.5	48.9	258	5	US-09-791-537-62042
11	624.5	48.9	264	5	US-09-791-537-91445
12	624.5	48.9	264	7	US-60-360-039-18839
13	610	47.8	256	7	US-60-360-039-21754
14	591	46.3	254	7	US-60-360-039-17909
15	591	46.3	261	7	US-60-360-039-11750
16	591	46.3	261	7	US-60-360-039-14291
17	591	46.3	261	7	US-60-360-039-14486
18	591	46.3	261	7	US-60-360-039-14870
19	589	46.1	272	7	US-60-360-039-12287
20	586	45.9	254	7	US-60-360-039-20612
21	581	45.5	264	7	US-60-360-039-7881
22	578	45.3	261	7	US-60-360-039-10861
23	575	45.0	250	7	US-60-360-039-18344
24	572.5	44.8	258	5	US-09-791-537-44256
25	572.5	44.8	278	5	US-09-791-537-29789
26	572.5	44.8	278	7	US-60-360-039-2640

ALIGNMENTS

RESULT 1  
US-09-791-537-111094  
; Sequence 111094, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Blonomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 111094  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-791-537-111094

Query Match 100.0%; Score 1277; DB 5; Length 256;  
Best Local Similarity 100.0%; Pred. No. 2.5e-105;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLNLENTYVIMGIANKRSTAFGVAKVLDQGLAKLVFTYRKRSRKELEKLEQLNQPEA 60  
Db 1 MLNLENTYVIMGIANKRSTAFGVAKVLDQGLAKLVFTYRKRSRKELEKLEQLNQPEA 60  
QY 61 HLVDQSDDEEVINGEQIGKDVGNIDGVYHSTAFANNEDLGRFSETSGEFLLAQDI 120  
Db 61 HLVDQSDDEEVINGEQIGKDVGNIDGVYHSTAFANNEDLGRFSETSGEFLLAQDI 120  
QY 121 SSSSLTVAHEAKKLMPGEGGSIVATTYLGGEFAVQNTVMGVAKASLEANKYKYLALDLP 180  
Db 121 SSSSLTVAHEAKKLMPGEGGSIVATTYLGGEFAVQNTVMGVAKASLEANKYKYLALDLP 180  
QY 181 DNIIRVNAISAGPRTILSAKGVGGFNTTLKETEERAPLKRNVQDQVEVGKTAAYLLSSG 240  
Db 181 DNIIRVNAISAGPRTILSAKGVGGFNTTLKETEERAPLKRNVQDQVEVGKTAAYLLSSG 240  
QY 241 VTGENIHVDSGFHAIK 256  
Db 241 VTGENIHVDSGFHAIK 256

RESULT 2  
US-10-089-019-12  
; Sequence 12, Application US/10089019

## ; GENERAL INFORMATION:

; APPLICANT: DEWOLF, WALTER E. JR  
; APPLICANT: KALLENDER, HOWARD  
; APPLICANT: LONSDALE, JOHN T.  
; TITLE OF INVENTION: METHODS FOR MAKING AND USING FAULTY ACID  
; TITLE OF INVENTION: SYNTHESIS PATHWAY REAGENTS

; FILE REFERENCE: GM50068

; CURRENT APPLICATION NUMBER: US/10/089,019

; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER: PCT/US00/29451

; PRIOR FILING DATE: 2000-10-26

; PRIOR APPLICATION NUMBER: 60/161,775

; PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 255

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-10-089-019-12

Query Match 98.9%; Score 1263; DB 6; Length 255;

Best Local Similarity 100.0%; Pred. No. 4.3e-104;

Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEAH 61

Db 3 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEAH 62

Qy 62 LYQIDVQSDVEEVINGFEQIGKDVGNIDGYHSAFANMEDLGRFSETSRGFLAQDIS 121

Db 63 LYQIDVQSDVEEVINGFEQIGKDVGNIDGYHSAFANMEDLGRFSETSRGFLAQDIS 122

Qy 122 SYSLSIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAKASLEANVYLALDIDPD 181

Db 123 SYSLSIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAKASLEANVYLALDIDPD 182

Qy 182 NIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQVEVGKTAAYLLSLDSGV 241

Db 183 NIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQVEVGKTAAYLLSLDSGV 242

Qy 242 TGENIHVDSGFHA 254

Db 243 TGENIHVDSGFHA 255

## RESULT 3

US-10-138-701-6

; Sequence 6, Application US/10138701

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides

; FILE REFERENCE: P484

; CURRENT APPLICATION NUMBER: US/10/138,701

; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: US/09/512,255A

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/098,964

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: US 60/009,861

; PRIOR FILING DATE: 1996-01-05

; PRIOR APPLICATION NUMBER: PCT/ US99/19726

; PRIOR FILING DATE: 1999-08-31

; PRIOR APPLICATION NUMBER: US 08/956,171

; PRIOR FILING DATE: 1997-10-20

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 256

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-10-138-701-6

Query Match 90.5%; Score 1156; DB 6; Length 256;

Best Local Similarity 87.9%; Pred. No. 1.4e-94;

Matches 239; Conservative 0; Mismatches 1; Indels 32; Gaps 2;

Qy 1 MLNENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEA 60

Db 1 MLNENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEA 60

Qy 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGYHSAFANMEDLGR 104

Db 61 HLYQIDVQSDVEEVINGFEQIGKDVGNIDGYHSAFANMEDLGR 104

Qy 105 RFSETSRGFLAQDISYSLSIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAK 164

Db 105 RFSETSRGFLAQDISYSLSIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAK 164

Qy 165 ASLEANVYLALDIDPDNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQV 224

Db 165 ASLEANVYLALDIDPDNIRVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQV 224

Qy 225 EVGKTAAYLLSLDSGVTGENIHVDSGFHA 256

Db 225 EVGKTAAYLLSLDSGVTGENIHVDSGFHA 256

## RESULT 4

US-60-360-039-16488

; Sequence 16488, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 16488

; LENGTH: 259

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-60-360-039-16488

Query Match 62.3%; Score 796; DB 7; Length 259;

Best Local Similarity 63.6%; Pred. No. 1.4e-62;

Matches 159; Conservative 38; Mismatches 53; Indels 0; Gaps 0;

Qy 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLLLEQLNQPEAH 63

Db 9 LQKTFVYVGVANOKSIAGIARSLHNAKLIIFTYAGERLERNVRELADTLEGOESLV 68

Qy 64 QIDVQSDVEEVINGFEQIGKDVGNIDGYHSAFANMEDLGRFSETSRGFLAQDIS 123

Db 69 PCDVTNDEELTACFETIKQEVGTIHGVAHCFAFANRDLKGEFVDTSRDGLLAQNISAF 128

Qy 124 SLTIVAHEAKKLMPEGSIVATYLGGEFAVQNYNMGVAKASLEANVYLALDIDPD 183

Db 129 SLTAVAREAKKVMTEGGNLTLYLGGERVVKNYVNMVAKASLEASVKYLANDLGQHG 188

Qy 184 RVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQVEVGKTAAYLLSLDSGVTG 243

Db 189 RVNAISAGPIRTLSAKGVGFNTILKEIERAPLKRNVQVEVGKTAAYLLSLDSGVTG 248

Qy 244 ENIHVDGFGH 253

Db 249 ENIHVDGFGH 258

RESULT 5  
US-60-360-039-17364  
; Sequence 17364, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 17364  
; LENGTH: 260  
; TYPE: PRT  
; ORGANISM: Bacillus halodurans  
US-60-360-039-17364

Query Match 60.1%; Score 767; DB 7; Length 260;  
Best Local Similarity 60.6%; Pred. No. 5.2e-60;  
Matches 154; Conservative 41; Mismatches 59; Indels 0; Gaps 0;  
QY 2 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLEQLNOPEAHL 61  
DB 4 LSLVDRTYVVMGVANKRSIAWGIAQSLANAGARLIIFTYAGERLEKNVGRGLVETLDRDHL 63  
QY 62 LQIDVOSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGREGFLAODISS 121  
DB 64 VLECDVTSDEAVEATPASKIEQVGTTHGLAHCIATFANKEELGELYLNTTRDGFLLAHNIS 123  
QY 122 SYSLTVAHEAKKLMPGGGSIVATTYLGGEFAVONVNMVGVAKASLEAVNYKYLALDLGPD 181  
DB 124 AVSLTAVAKAARPLMNEGSIIVTLTGGEKVVRNVNMVGVAKASLDASVKYLANDLGRKE 183  
QY 182 NIRVNAISAGPIRTLSAKGVGGFNTILKEERAPLRNVDOVEVGKTAAYLLSDLSGGV 241  
DB 184 NIRVNAISAGPIRTLSAKGVGGFNTILKEERAPLRNVDOVEVGKTAAYLLSDLSGGV 241  
QY 242 TGENIHVDSGFHAI 255  
DB 244 TGEILHVDSGYNIL 257

RESULT 6  
US-09-791-537-130900  
; Sequence 130900, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 130900  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
US-09-791-537-130900  
Query Match 58.7%; Score 749; DB 5; Length 258;  
Best Local Similarity 59.0%; Pred. No. 2e-58;  
Matches 148; Conservative 41; Mismatches 62; Indels 0; Gaps 0;

QY 3 NLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLEQLNOPEAHL 62  
DB 4 SLEGRNIVVMGVANKRSIAWGIAQSLANAGARLIIFTYAGERLEKNVGRGLVETLDRDHL 63  
QY 63 YQIDVOSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGREGFLAODISS 122  
DB 64 LQCDVTNDAAIEITCFASIKQVGVHGIACHIAFANKEELVGEYLNTRDGFLLAHNIS 123  
QY 123 YSLTVAHEAKKLMPGGGSIVATTYLGGEFAVONVNMVGVAKASLEAVNYKYLALDLGPD 182  
DB 124 AVSLTAVAKAARPLMNEGSIIVTLTGGEKVVRNVNMVGVAKASLDASVKYLANDLGRKE 183  
QY 183 IRVNAISAGPIRTLSAKGVGGFNTILKEERAPLRNVDOVEVGKTAAYLLSDLSGGV 242  
DB 184 IRVNAISAGPIRTLSAKGVGGFNTILKEERAPLRNVDOVEVGKTAAYLLSDLSGGV 242  
QY 243 GENIHVDSGFH 253  
DB 244 GENLHVDSGFH 254

RESULT 7  
US-09-791-537-2330  
; Sequence 2330, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2330  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
US-09-791-537-2330  
Query Match 58.7%; Score 749; DB 5; Length 269;  
Best Local Similarity 59.0%; Pred. No. 2.2e-58;  
Matches 148; Conservative 41; Mismatches 62; Indels 0; Gaps 0;  
QY 3 NLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKRSRKELEKLEQLNOPEAHL 62  
DB 15 SLEGRNIVVMGVANKRSIAWGIAQSLANAGARLIIFTYAGERLEKNVGRGLVETLDRDHL 74  
QY 63 YQIDVOSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSGREGFLAODISS 122  
DB 75 LQCDVTNDAAIEITCFASIKQVGVHGIACHIAFANKEELVGEYLNTRDGFLLAHNIS 134  
QY 123 YSLTVAHEAKKLMPGGGSIVATTYLGGEFAVONVNMVGVAKASLEAVNYKYLALDLGPD 182  
DB 135 YSLTAVAKAARPLMNEGSIIVTLTGGEKVVRNVNMVGVAKASLDASVKYLANDLGRKE 194  
QY 183 IRVNAISAGPIRTLSAKGVGGFNTILKEERAPLRNVDOVEVGKTAAYLLSDLSGGV 242  
DB 195 IRVNAISAGPIRTLSAKGVGGFNTILKEERAPLRNVDOVEVGKTAAYLLSDLSGGV 242  
QY 243 GENIHVDSGFH 253  
DB 255 GENLHVDSGFH 265

RESULT 8  
US-60-360-039-17696  
; Sequence 17696, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 17696  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
US-60-360-039-17696

Query Match 58.7%; Score 749; DB 7; Length 269;  
Best Local Similarity 59.0%; Pred. No. 2.2e-58;  
Matches 148; Conservative 41; Mismatches 62; Indels 0; Gaps 0;

Qy 3 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTYRKSRKELEKLEQLNOPEAHL 62  
Db 15 SLEGNVVMGVANKRSTAWGARSLEHAGARLFTYAGERLEKSVHELACTLDRNDSII 74  
Qy 63 YQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSREGFLLAQDISS 122  
Db 75 LPCDVTDAETCTFASIKQGVGTHGIAHCFATFANKBELVGEYLTNRDGFLLAHNISS 134  
Qy 123 YSLRTVAHEAKLMPEGGSIATVTLGGGFVAVQNYVMGVAKASLEANKVYLALDGLPDN 182  
Db 135 YSLTAVKAAAPMTGGSIATVTLGGELVMPNYVMGVAKASLDASVKYLAADLCKEN 194  
Qy 183 IRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSGGVT 242  
Db 195 IRVNSISAGPIRTLSAKGISDFNSILKDIERAPLRRTTPEEVGDTAAFLFSDMSRGIT 254  
Qy 243 GENTHVDSGFH 253  
Db 255 GENTHVDSGFH 265

RESULT 9  
US-60-360-039-20054  
; Sequence 20054, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 20054  
; LENGTH: 260  
; TYPE: PRT  
; ORGANISM: Nostoc punctiforme  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(260)  
; OTHER INFORMATION: unsure at all xaa locations  
US-60-360-039-20054

Query Match 49.1%; Score 626.5; DB 7; Length 260;  
Best Local Similarity 52.5%; Pred. No. 1.6e-47;  
Matches 134; Conservative 45; Mismatches 71; Indels 5; Gaps 3;

Qy 1 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTY---RKERSRKELEKLEQLNQ 57  
Db 11 SLEGNVVMGVANKRSTAWGARSLEHAGARLFTYAGERLEKSVHELACTLDRNDSII 74

Db 3 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTYRKSRKELEKLEQLNOPEAHL 61  
Qy 58 PEALHYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSREGFLLA 117  
Db 62 PSFLF-PCNVQDEQIQSTFTIREQWGLDLILHCLAFASKDDLSGDFQSOTSRSGFSTA 120  
Qy 118 QDISSYSLTIVAHEAKLMPEGGSIATVTLGGGFVAVQNYVMGVAKASLEANKVYLALD 177  
Db 121 LEISTYSLVOLSGAAKPLMTGGSIATVTLGGVRAIPNYVMGVAKAGLEASVRYLAEE 180  
Qy 178 LGPDNIRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSD 237  
Db 181 LGPDNIRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSD 240  
Qy 238 SSGVTGENIHVDSGF 252  
Db 241 SSGVTGENIHVDAGY 255

RESULT 10  
US-09-791-537-62042  
; Sequence 62042, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 62042  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Anabaena PCC7120  
US-09-791-537-62042

Query Match 48.9%; Score 624.5; DB 5; Length 258;  
Best Local Similarity 52.2%; Pred. No. 2.3e-47;  
Matches 133; Conservative 47; Mismatches 70; Indels 5; Gaps 3;

Qy 1 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTY---RKERSRKELEKLEQLNQ 57  
Db 1 MLNLTGKALVTGIANNRSTAFGAKVLDGAKLVFTYRKSRKELEKLEQLNQ 59  
Qy 58 PEALHYQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRFSETSREGFLLA 117  
Db 60 PSFLF-PCNVQDEQIQSTFTIREQWGLDLILHCLAFASKDDLSGDFQSOTSRSGFSTA 118  
Qy 118 QDISSYSLTIVAHEAKLMPEGGSIATVTLGGGFVAVQNYVMGVAKASLEANKVYLALD 177  
Db 119 LDISTFSLVOLSGAAKPLMTGGSIATVTLGGVRAIPNYVMGVAKAGLEASVRYLAEE 178  
Qy 178 LGPDNIRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSD 237  
Db 179 LGPDNIRVNAISAGPIRTLSAKGVGGFTILKEIEERAPLKRNVDOVEVGKTAAYLLSD 238  
Qy 238 SSGVTGENIHVDSGF 252  
Db 239 SSGVTGENIHVDAGY 253

RESULT 11  
US-09-791-537-91445  
; Sequence 91445, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91445
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Nostoc sp
US-09-791-537-91445

Query Match 48.9%; Score 624.5; DB 5; Length 264;
Best Local Similarity 52.2%; Pred. No. 2.4e-47;
Matches 133; Conservative 47; Mismatches 70; Indels 5; Gaps 3;

QY 1 MLNLENTYVIMGIANKRSITAFGKLVYAKVLDQGLAKLVFTY---RKERSRKELEKLLLEQLNQ 57
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 7 MLNLTGKNAVLTGIANNRSIANGIAQOLHAAGANLIGITYLPDRGKFEKVKVSELVEPLN- 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 58 PEARLQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSHAFANMEDLRGRFSETSGREGFLA 117
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 66 PSFL-PCNVQNDQIQSTFTDIRDKWGRDLILHCLAFANRDLDTGDFSTQTSRAGFATA 124
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 118 QDISSTSLTIVAHEAKLMPEGGSIATVYLGGEFAVQNTVNMGVAKASLEANKYALD 177
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 125 LDISTFSLVOLSGAAKPLMTEGGSIIITLSYLGGRVAVPNTVNMGVAKASLEANSVRYLASE 184
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 178 LGPDNRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDL 237
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 185 LGSQNRVNAISAGPIRTLASSAVGGILDMHHVEQVA2LRRTVTQLEVGNTAAFLASDL 244
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 238 SSGVTGENIHVDSGF 252
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 245 ASGITGVLYVDAGY 259
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

RESULT 12
US-60-360-039-18839
; Sequence 18839, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18839
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Anabaena PCC7120
US-60-360-039-18839

Query Match 48.9%; Score 624.5; DB 7; Length 264;
Best Local Similarity 52.2%; Pred. No. 2.4e-47;
Matches 133; Conservative 47; Mismatches 70; Indels 5; Gaps 3;

QY 1 MLNLENTYVIMGIANKRSITAFGKLVYAKVLDQGLAKLVFTY---RKERSRKELEKLLLEQLNQ 57
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 7 MLNLTGKNAVLTGIANNRSIANGIAQOLHAAGANLIGITYLPDRGKFEKVKVSELVEPLN- 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 58 PEARLQIDVQSDVEEVINGFEQIGKDVGNIDGVYHSHAFANMEDLRGRFSETSGREGFLA 117
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 66 PSFL-PCNVQNDQIQSTFTDIRDKWGRDLILHCLAFANRDLDTGDFSTQTSRAGFATA 124
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 118 QDISSTSLTIVAHEAKLMPEGGSIATVYLGGEFAVQNTVNMGVAKASLEANKYALD 177
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 125 LDISTFSLVOLSGAAKPLMTEGGSIIITLSYLGGRVAVPNTVNMGVAKASLEANSVRYLASE 184
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 178 LGPDNRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDL 237
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 185 LGSQNRVNAISAGPIRTLASSAVGGILDMHHVEQVA2LRRTVTQLEVGNTAAFLASDL 244
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 238 SSGVTGENIHVDSGF 252
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 245 ASGITGVLYVDAGY 259
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

RESULT 13
US-60-360-039-21754
; Sequence 21754, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21754
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Rhodobacter capsulatus
US-60-360-039-21754

Query Match 47.8%; Score 610; DB 7; Length 256;
Best Local Similarity 49.8%; Pred. No. 4.5e-46;
Matches 125; Conservative 44; Mismatches 81; Indels 2; Gaps 1;

QY 4 LENKTYVIMGIANKRSITAFGKLVYAKVLDQGLAKLVFTYRKRSRKELEKLLLEQLNOPEARHLY 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 6 MAGKRGILMGLANDKSIANGIAKALGADAGAEAFSYGHEALKKRVEPLAASLGTP--LLF 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 64 QIDVQSDVEEVINGFEQIGKDVGNIDGVYHSHAFANMEDLRGRFSETSGREGFLAQQDISY 123
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 64 ECDVANEDSDALFAGLKDAGWTLDLVYHAIQFSDKNELRGYVDTSRGNFTMTDISVY 123
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 124 SLTIVAHEAKLMPEGGSIATVYLGGEFAVQNTVNMGVAKASLEANKYALDLDPDNI 183
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 124 SFTAVCARAAAMPNGSGSLTLYTGAEQVMPHYNMVGVAKAALASVYKTYAEDLKLGI 183
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDOVEVGKTAAYLLSDLSSGVTG 243
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 184 RCNAISAGPIKTLAASGIGDFRYIMKNWLNPLRRNVQEEVGKAAALYLLSDLSGSGTG 243
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 244 ENIHVDSGFPHAI 255
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 244 ENLHVDAHYHV 255
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

RESULT 14
US-60-360-039-17909
; Sequence 17909, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 15:11:13 ; Search time 47.08 Seconds  
(without alignments)  
4022.588 Million cell updates/sec

Title: US-09-292-411a-1  
Perfect score: 771  
Sequence: 1 atgttaaatcttgaaacaa.....gattccacgcgaattaaataa 771

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54.2	7.0	1173	4	US-09-586-719-1
2	50.2	6.5	741	3	US-09-238-481-1
3	41.4	5.4	4198	4	US-09-586-719-11
4	39.4	5.1	3763	1	US-07-792-865D-1
5	39.2	5.1	797	2	US-08-752-132-1
6	39	5.1	1891	4	US-08-973-462-3
7	39	5.1	5361	4	US-08-973-462-2
8	39	5.1	6152	4	US-08-973-462-1
9	38.8	5.0	951	4	US-09-241-750-1
10	38	4.9	5910	1	US-08-195-814-1
11	38	4.9	7218	1	US-08-232-463-14
12	37.6	4.9	1251	3	US-09-007-476-1
13	37.6	4.9	2483	1	US-08-526-964-1
14	37.6	4.9	2483	2	US-08-946-617-1
15	37.6	4.9	2483	3	US-09-031-897-1
16	37.6	4.9	5203	4	US-09-257-770-1
17	37.2	4.8	7493	1	US-08-212-133A-7
18	37.2	4.8	7493	1	US-08-474-503-5
19	37.2	4.8	7493	2	US-08-670-707A-5
20	37.2	4.8	7493	4	US-09-037-601-5
21	37.2	4.8	7493	5	PCT-US94-13200-5
22	36.8	4.8	824	1	US-08-158-353-1
23	36	4.7	2301	4	US-09-561-825-1
24	36	4.7	2361	4	US-09-561-825-26
25	36	4.7	2361	4	US-09-561-825-29
26	36	4.7	2362	4	US-09-561-825-27
27	36	4.7	2363	4	US-09-561-825-28

28	35.8	4.6	2101	2	US-08-568-459A-9	Sequence 9, Appl
29	35.8	4.6	2101	2	US-08-487-826B-9	Sequence 9, Appl
30	35.8	4.6	7295	2	US-08-487-826B-15	Sequence 15, Appl
31	35.6	4.6	654	4	US-08-936-165A-234	Sequence 234, App
32	35.6	4.6	1431	4	US-09-316-083-2	Sequence 2, Appl
33	35.4	4.6	7101	1	US-08-480-604A-9	Sequence 9, Appl
34	35.4	4.6	7101	2	US-08-405-496A-9	Sequence 9, Appl
35	35.4	4.6	7101	4	US-08-915-136-9	Sequence 9, Appl
36	35.2	4.6	1830	2	US-08-933-750C-79	Sequence 79, Appl
37	35.2	4.6	1830	3	US-09-234-613-79	Sequence 79, Appl
38	35	4.5	1601	3	US-09-038-909-1	Sequence 1, Appl
39	35	4.5	3879	1	US-08-530-010-1	Sequence 1, Appl
40	35	4.5	3879	1	US-08-484-101B-1	Sequence 1, Appl
41	35	4.5	3879	4	US-08-714-524D-1	Sequence 1, Appl
42	35	4.5	5319	1	US-08-169-927-1	Sequence 1, Appl
43	34.8	4.5	1500	4	US-08-856-253-5	Sequence 5, Appl
44	34.8	4.5	3827	2	US-08-447-031A-1	Sequence 1, Appl
45	34.8	4.5	4612	2	US-08-447-031A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1  
US-09-586-719-1  
; Sequence 1, Application US/09586719  
; Patent No. 6294345  
; GENERAL INFORMATION:  
; APPLICANT: Zheng, Feng  
; APPLICANT: Levin, Joshua Z.  
; APPLICANT: Bauer, Michael W.  
; TITLE OF INVENTION: Herbicide Target Genes and Methods  
; FILE REFERENCE: PB/5-30909A  
; CURRENT APPLICATION NUMBER: US/09/586,719  
; CURRENT FILING DATE: 2000-06-05  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1173)  
US-09-586-719-1

Query Match 7.0%; Score 54.2; DB 4; Length 1173;  
Best Local Similarity 52.5%; Pred.No. 8.5e-06;  
Matches 116; Conservative 1; Mismatches 104; Indels 0; Gaps 0;

QY	544	aatttcggttaattcaatttcagctggtcccaatcgctacattagtgcaaaaggtgtg	603
Db	901	aacattagggtcaacaccatatctcggttcctttgggaagcgcagcaaaagccatt	960
QY	604	ggtggttcatacaattcttaaaagaatcgagagcgtgacaccttaaacgttaacgtt	663
Db	961	gggttcatagacaccatgattgagtattcctcaataaaggacctattcagaaaacactg	1020
QY	664	gatcaagtgaagttagtaaaacacagcggcttacttttaagtgaacttatcaagtgcgtt	723
Db	1021	accgcagagaaggttggaatgacagcctctcttgccattggcctctgcata	1080
QY	724	acaggtgaaaaattattcatgtagatagcggattccacgcaat	764
Db	1081	accggtgcaaccatatatgtggacaatggtttgaatgcaat	1121

RESULT 2  
US-09-238-481-1  
; Sequence 1, Application US/09238481  
; Patent No. 6110704  
; GENERAL INFORMATION:

```

; APPLICANT: Huang, Jianzhong
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Fabg
; FILE REFERENCE: GM10192
; CURRENT APPLICATION NUMBER: US/09/238,481
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; US-09-238-481-1

Query Match      6.5%   Score 50.2; DB 3; Length 741;
Best Local Similarity 48.0%; Pred. No. 8.8e-05;
Matches 176; Conservative 1; Mismatches 184; Indels 6; Gaps 1;

Qy 393 agctaaaaaattaatgccagaggtggtgtagcattgttgcaacaacatatatttagtggtgcga 452
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 accacaaatgtaagacaaacgtagtggtgctcatcatcaatttatcaagtggtgtggagc 434

Qy 453 attcgcggttcaaaattataatgtgtggtggtggtggtggtggtggtggtggtggtggtggt 512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 435 agtaggtaaatccgggacaaagcaaaactatgttgcaaaaaagcaggtgtgtattggtttaac 494

Qy 513 taatatttagcattagcattagtcctgataatatttcggttaattgtaattcagctgg 572
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 495 taaatcggcggcgtgaattagcattcgtcgtggtcactgtaaatgagtcagtcacctgg 554

Qy 573 tccaatcgtacattagtcgcaaaaggtggtggtggtggtggtggtggtggtggtggtggtggt 632
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 555 ttttattgttctgatatgacagatgtcttaagt-----atgagcttaaaagacaaat 608

Qy 633 cgaagagcgtgcaccttttaaaacacgttgatcaagtagaagtaggtaaaacacagcggc 692
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 609 gttgactcaaatccgttagcgtgttgggtcgaagacacagatattgctaatacagtagc 668

Qy 693 ttacttttaagtacttatcaagtgcgttacaggtgaaataattctatgtagatagcg 752
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 669 gttcttagcatcagacaaaagcaaaatattacaggttcaacaacatccatgtaaatggtg 728

Qy 753 attccac 759
   ||| |||
Db 729 aatgtac 735

RESULT 3
US-09-586-719-11
; Sequence 11, Application US/09586719
; Patent No. 6294345
; GENERAL INFORMATION:
; APPLICANT: Zheng, Feng
; APPLICANT: Levin, Joshua Z.
; APPLICANT: Bauer, Michael W.
; TITLE OF INVENTION: Herbicide Target Genes and Methods
; FILE REFERENCE: PB/5-30909A
; CURRENT APPLICATION NUMBER: US/09/586,719
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 4198
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-586-719-11

Query Match      5.4%   Score 41.4; DB 4; Length 4198;
Best Local Similarity 59.0%; Pred. No. 0.04;
Matches 69; Conservative 1; Mismatches 47; Indels 0; Gaps 0;

Qy 648 tttaaacgtaacgttgatcaagtagaagtaggtaaaacagcggcttacttrttaagtga 707
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3317 tttaataatggcgatgatgtagatgaagttgggaatgcagcagcttcttggcatctcc 3376

Qy 708 cttatcaagtggtggtttacaggtgaaataattcattgtagatagcggattccacgcaat 764
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3377 attgctctgcataaccggtgcaaccatattgtggaacatgtgttggaatggaatgcaat 3433

; APPLICANT: John W. Barnwell, Mary W. Galinski,
; APPLICANT: Samuel P. Wertheimer
; TITLE OF INVENTION: MEROZOITE ANTIGENS LOCALIZED AT
; TITLE OF INVENTION: THE APICAL END OF THE PARASITE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM or IBM-compatible
; OPERATING SYSTEM: PC/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/792,865D
; FILING DATE: 19911004
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/01849
; FILING DATE: April 3, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson, Arthur
; REGISTRATION NUMBER: 34,354
; REFERENCE/DOCKET NUMBER: 5986/14692-US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3763 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; DESCRIPTION:
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: P.vivax
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY: Lambda gt 11 native P.vivax
; LIBRARY: DNA expression library
; CLONE: 5.3
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
```









TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 622-8200  
TELEFAX: (216) 241-0816  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2483 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-08-526-964-1

Query Match 4.9%; Score 37.6; DB:1; Length 2483;  
Best Local Similarity 47.1%; Pred. No. 0.35;  
Matches 115; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 2 ttttaaatcttgaacacacataatgtcatcgtggaatcgctaaataagcgtagtattg 61  
DB 1096 TATTAAATGAGAGATCAAGATCAAGTTTCATAGACTTATTATATAAATTTAAGAG 1155  
QY 62 ctttgggtgcgtaagtttttagatcaattaggtgctaaatagttattactaccgta 121  
DB 1156 CTGGATATGTTGATAAAATAATAATATCATAATACAACTTTAGGAATCTCAAGGTA 1215  
QY 122 aagaacgtagcgcgaagcgttgaaaaattattagaacaaataaaatcaaccagaagcgc 181  
DB 1216 GTGTTGTCAGTCTCTATTTTATGTAATATTTTTTTAGATAAATAGATAAATTTAGAAA 1275  
QY 182 acttatcaaatgttgctcaaacgatgaagaggttattaatggttttgacaaattg 241  
DB 1276 ATAAATTTGAGATGAATCAACTACTGGAATATGCTAATAGAGGTAGAGATCAATTT 1335  
QY 242 gtaa 245  
DB 1336 ATAA 1339

## RESULT 14

US-08-946-617-1  
Sequence 5, Application US/08911320A  
Patent No. 5869633  
GENERAL INFORMATION:  
APPLICANT: INCYTE PHARMACEUTICALS, INC.  
TITLE OF INVENTION: THROMBIN RECEPTOR HOMOLOG  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,320A  
FILING DATE: August 14, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/467,125  
FILING DATE: 6-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0041-1 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-845-4170  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 25  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
Sequence 1, Application US/08946617  
Patent No. 5869634  
GENERAL INFORMATION:  
APPLICANT: Lambowitz, Alan M  
APPLICANT: Zimmerly, Steven  
APPLICANT: Guo, Huatao  
APPLICANT: Yang, Jian  
TITLE OF INVENTION: Nucleotide Integrase Preparation  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calfee, Halter & Griswold  
STREET: 800 Superior Avenue  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: USA  
ZIP: 44114  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/946,617  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gorrlick, Mary E  
REGISTRATION NUMBER: 34,829  
REFERENCE/DOCKET NUMBER: 22727/00127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 622-8200  
TELEFAX: (216) 241-0816  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2483 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-08-946-617-1

Query Match 4.9%; Score 37.6; DE 2; Length 2483;  
Best Local Similarity 47.1%; Pred. No. 0.35;  
Matches 115; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 2 ttttaaatcttgaacacacacataatgtcatcgtggaatcgctaaataagcgtagtattg 61  
DB 1096 TATTAAATGAGAGATCAAGATCAAGTTTCATAGACTTATTATATAAATTTAAGAG 1155  
QY 62 ctttgggtgcgctaaagtttttagatcaattaggtgctaaatagttattactaccgta 121  
DB 1156 CTGGATATGTTGATAAAATAATAATATCATAATACAACTTTAGGAATCTCAAGGTA 1215  
QY 122 aagaacgtagcgcgaagcgttgaaaaattattagaacaaataaaatcaaccagaagcgc 181  
DB 1216 GTGTTGTCAGTCTCTATTTTATGTAATATTTTTTTAGATAAATAGATAAATTTAGAAA 1275  
QY 182 acttatcaaatgttgctcaaacgatgaagaggttattaatggttttgacaaattg 241  
DB 1276 ATAAATTTGAGATGAATCAACTACTGGAATATGCTAATAGAGGTAGAGATCAATTT 1335  
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Search completed: September 22, 2002, 16:07:00  
Job time: 3347 sec

RESULT 15  
US-09-031-897-1  
; Sequence 1, Application US/09031897  
; Patent No. 6027895  
; GENERAL INFORMATION:  
; APPLICANT: Lambowitz, Alan  
; APPLICANT: Mohr, Georg  
; APPLICANT: Zimmerly, Steven  
; APPLICANT: Guo, Huatao  
; TITLE OF INVENTION: Methods Cleaving DNA with Nucleotide  
; TITLE OF INVENTION: Integrases  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calfee, Halter & Griswold  
; STREET: 800 Superior Avenue, Suite 1400  
; CITY: Cleveland  
; STATE: Ohio  
; COUNTRY: US  
; ZIP: 44114  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/031.897  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Docherty, Pamela A.  
; REGISTRATION NUMBER: 40,591  
; REFERENCE/DOCKET NUMBER: 24671/00105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (216)622-8416  
; TELEFAX: (216)241 0816  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2483 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; US-09-031-897-1

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Qy 242 gtaa 245  
Db 1336 ATAA 1339



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 15:12:28 ; Search time 2795.16 Seconds  
(without alignments)  
5967.639 Million cell updates/sec

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Perfect score: 771  
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Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	770.6	99.9	771	11	US-08-790-043A-2
3	770.6	99.9	771	11	US-08-790-043A-2
4	770.6	99.9	771	16	US-09-292-411A-1
5	770.6	99.9	771	16	US-09-292-411A-1
6	770.6	99.9	771	16	US-09-292-411A-1
7	767.6	99.6	774	1	PCT-US00-29451-11
8	762.6	98.9	771	1	PCT-US02-03987-8794
9	762.6	98.9	771	31	US-09-815-242-8794
10	762.6	98.9	771	37	US-10-072-851-8794
11	761	98.7	916	1	PCT-US99-19726-5
12	761	98.7	916	19	US-09-512-255-5
13	761	98.7	916	19	US-09-512-255-5
14	756.6	98.1	775	1	PCT-US00-12104-1
15	756.6	98.1	775	37	US-10-009-219-1
16	755.6	98.0	1167	1	PCT-US97-02318-1110
17	755.6	98.0	1167	13	US-08-903-470-1110
18	749.8	97.3	771	1	PCT-US02-03987-8437
19	749.8	97.3	771	31	US-09-815-242-8437
20	749.8	97.3	771	37	US-10-072-851-8437
21	746.8	96.9	768	1	PCT-US02-03987-4173
22	746.8	96.9	768	31	US-09-815-242-4173
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26	743	96.4	278942	23	US-09-611-529-7437
27	734.6	95.3	77711	12	US-08-831-156A-105
28	645	83.7	704	11	US-08-781-986A-772
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31	645	83.7	704	13	US-08-956-171C-772

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33	33	546.6	70.9	783	15	US-09-134-001C-117
34	34	546.6	70.9	783	18	US-09-450-969-2044
35	35	539.2	69.9	560	24	US-09-620-608-111
36	36	539.2	69.9	560	53	US-60-144-883-111
37	37	535.2	69.4	15846	45	US-60-068-228-373
38	38	535.2	69.4	15852	43	US-60-046-933-370
39	39	535.2	69.4	26773	42	US-60-038-081-389
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c 42	c 42	456	59.1	552	31	US-09-815-242-1952
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## ALIGNMENTS

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; Sequence 2, Application US/08790043
; GENERAL INFORMATION:
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: Novel Fabi
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,043
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024845
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: GMS0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-790-043-2

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	Best Local Similarity	100.0%;	Pred. No. 1.8e-177;		
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; Sequence 2, Application US/08790043A
; GENERAL INFORMATION:
; APPLICANT: 'Lonsdale'
; APPLICANT: Milner, John
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: Novel Fabi
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/790,043A  
FILING DATE: 28-August-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/024845  
FILING DATE: 28-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Glimm, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: GM50005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 771 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-08-790-043A-2

Query Match 99.9%; Score 770.6; DB 11; Length 771;  
Best Local Similarity 100.0%; Pred. No. 1.8e-177; Mismatches 0; Indels 0; Gaps 0;  
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Sequence 1, Application US/08790043B  
GENERAL INFORMATION:  
APPLICANT: Payne, David  
APPLICANT: Lonsdale, John  
APPLICANT: Milner, Peter  
APPLICANT: Pearson, Stewart  
TITLE OF INVENTION: FAB I  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dechert Price & Rhoads  
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
CITY: Philadelphia  
STATE: PA  
COUNTRY: US  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA: US/08/790,043B  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/024,845  
FILING DATE: 28-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Falk, Stephen T  
REGISTRATION NUMBER: 36,795  
REFERENCE/DOCKET NUMBER: GM50005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-994-2488  
TELEFAX: 215-994-2222  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 771 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-790-043B-1

Query Match 99.9%; Score 770.6; DB 11; Length 771;  
Best Local Similarity 100.0%; Pred. No. 1.8e-177; Mismatches 0; Indels 0; Gaps 0;  
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 atgttaaaattgaaacaaacatatgtcatcattggaatcgtaataagcgtagtatt 60  
DB 1 ATGTTAAATCTTGAAACAAACATATGTCATCGGATCGCTAATAAGCGTAGTATT 60  
QY 61 gctttgggtgcctaaagtcttagatcaattaggtgctaaattagttactaccgt 120  
DB 61 GCTTTGGTGCCTAAAGTTTGTAGTCAATTAGTGTCTAAATAGTATTACTTACCGT 120  
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DB 181 CACTTATCAAAATGATGTTCAACGGATGAAGAGTTATTAAATGGTTTGAGCAAAAT 240



APPLICANT: Milner, Peter  
APPLICANT: Payne, David  
APPLICANT: Pearson, Stewart  
TITLE OF INVENTION: Fabi  
FILE REFERENCE: GM50005-D1  
CURRENT APPLICATION NUMBER: US/09/292,411A  
CURRENT FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: US 08/790,043  
PRIOR FILING DATE: 1997-01-28  
PRIOR APPLICATION NUMBER: US 60/024,845  
PRIOR FILING DATE: 1996-08-26  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 771  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-09-292-411A-1

Query Match 99.9%; Score 770.6; DB 16; Length 771;  
Best Local Similarity 100.0%; Pred. No. 1.8e-177;  
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaaatcttgaaacaaacataatgcatatggaatcgctaaatagcgtatgatt 60  
DB 1 atgttaaatcttgaaacaaacataatgcatatggaatcgctaaatagcgtatgatt 60

QY 61 gctttggtgctgctaaagtctttagatcaataggtgctaaatagctattaccgt 120  
DB 61 gctttggtgctgctaaagtctttagatcaataggtgctaaatagctattaccgt 120

QY 121 aaagaacgtagcgtgaaagcttgaaatattattagaacaattaaatcaaccagaagcg 180  
DB 121 aaagaacgtagcgtgaaagcttgaaatattattagaacaattaaatcaaccagaagcg 180

QY 181 caattatacaaatgattgttcaaacgcatgaagaggttattaaatggtttgagcaaat 240  
DB 181 caattatacaaatgattgttcaaacgcatgaagaggttattaaatggtttgagcaaat 240

QY 241 ggttaagatggtgcaaatattggtgctatcatcattcaatcgctaaatgctaaatgga 300  
DB 241 ggttaagatggtgcaaatattggtgctatcatcattcaatcgctaaatgctaaatgga 300

QY 301 gacttacgagcgtctttctgaaactcagctgaaggtctcttctgttagctcaagacatt 360  
DB 301 gacttacgagcgtctttctgaaactcagctgaaggtctcttctgttagctcaagacatt 360

QY 361 agttcttactcattaaacattggtgctcatgaagctaaatgctaaatgctaaatgctaa 420  
DB 361 agttcttactcattaaacattggtgctcatgaagctaaatgctaaatgctaaatgctaa 420

QY 421 agcattgttgcaacaacataattaggtggtgcaatctcgagttcgaatataatgctgag 480  
DB 421 agcattgttgcaacaacataattaggtggtgcaatctcgagttcgaatataatgctgag 480

QY 481 ggtgtgtctaaagcagcttagaagcaaatgtttaaataatttagcatttagcttccct 540  
DB 481 ggtgtgtctaaagcagcttagaagcaaatgtttaaataatttagcatttagcttccct 540

QY 541 gataattatcgcttaataatgcaatttcagctggtcccaatccgtacattagtgcaaaaggt 600  
DB 541 gataattatcgcttaataatgcaatttcagctggtcccaatccgtacattagtgcaaaaggt 600

QY 601 gtgggtgtgttcaatacaattcttaagaaatcgagagcggtgcaccttttaaacgtaac 660  
DB 601 gtgggtgtgttcaatacaattcttaagaaatcgagagcggtgcaccttttaaacgtaac 660

QY 661 gttgatcaagtagaagtagtaaaacagcggttactttrttaagtgtacttatacaagtgcc 720  
DB 661 gttgatcaagtagaagtagtaaaacagcggttactttrttaagtgtacttatacaagtgcc 720

QY 721 gttacaggtgaaataattcatgtagatagcggattccacgcgaattaaataa 771

DB 721 gttacaggtgaaataattcatgtagatagcggattccacgcgaattaaataa 771

RESULT 6  
US-09-292-412-1  
Sequence 1, Application US/09292412  
GENERAL INFORMATION:  
APPLICANT: Payne, David  
APPLICANT: Lonsdale, John  
APPLICANT: Milner, Peter  
APPLICANT: Pearson, Stewart  
TITLE OF INVENTION: FAB I  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Dechert Price & Rhoads  
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
CITY: Philadelphia  
STATE: PA  
COUNTRY: US  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/292,412  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/790,043  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Falk, Stephen T  
REGISTRATION NUMBER: 36,795  
REFERENCE/DOCKET NUMBER: GM50005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-994-2488  
TELEFAX: 215-994-2222  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 771 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-292-412-1

Query Match 99.9%; Score 770.6; DB 16; Length 771;  
Best Local Similarity 100.0%; Pred. No. 1.8e-177;  
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttaaatcttgaaacaaacataatgcatatggaatcgctaaatagcgtatgatt 60  
DB 1 atgttaaatcttgaaacaaacataatgcatatggaatcgctaaatagcgtatgatt 60

QY 61 gctttggtgctgctaaagtctttagatcaataggtgctaaatagctattaccgt 120  
DB 61 gctttggtgctgctaaagtctttagatcaataggtgctaaatagctattaccgt 120

QY 121 aaagaacgtagcgtgaaagcttgaaatattattagaacaattaaatcaaccagaagcg 180  
DB 121 aaagaacgtagcgtgaaagcttgaaatattattagaacaattaaatcaaccagaagcg 180

QY 181 caattatacaaatgattgttcaaacgcatgaagaggttattaaatggtttgagcaaat 240  
DB 181 caattatacaaatgattgttcaaacgcatgaagaggttattaaatggtttgagcaaat 240

QY 241 ggttaagatggtgcaaatattggtgctatcatcattcaatcgctaaatgctaaatgga 300  
DB 241 ggttaagatggtgcaaatattggtgctatcatcattcaatcgctaaatgctaaatgga 300

QY 301 gacttacgcggacgctttctgaaacttcaagtggaaggtcttctgttagctcaagacatt 360  
|||||  
Db 301 GACTTACGCGGACGCTTTCTGAAACTTCACGTGAAGGCTTCTGTAGCTCAAGACATT 360  
|||||  
QY 361 agttcttactcaataaacttgctgcatgaagctaaataaataatcccgagaaggtggt 420  
|||||  
Db 361 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTAAATAATTAATGCCAGAAGGTGT 420  
|||||  
QY 421 agcatgtgtgaacaacataatttaggtggaattcgcagttcgaataataataatgtagt 480  
|||||  
Db 421 AGCATGTGTGCAACAACAFATTTAGTGGCGAATTCGCGAGTTCAAAATTAATGTGTATG 480  
|||||  
QY 481 ggtgtgtgaagcgagcttagaagcaaatgttaataatttagcattagacttagtgcct 540  
|||||  
Db 481 GGTGTGTGCTGAAGCGAGCTTAGAAGCAAAATGTTAAATTTAGCATTAGACTTAGTCTCT 540  
|||||  
QY 541 gataataatcgcgttaataatgcgaatttcagctggtccaaatccgtacatttaagtcgaaggt 600  
|||||  
Db 541 GATAATATTCGCTTAAATGCAATTTACGCTGCTCCAAATCCGTACATTAAAGTCAAAAGGT 600  
|||||  
QY 601 gtgggtgtgttcaatacacaattcttaagaataatcgaagcgctgcaccttttaaacgtaac 660  
|||||  
Db 601 GTGGGTGTTTCAATACAAATCTTAAAGCAATTCGAAGACGCTGCACCTTTAAACGTAAC 660  
|||||  
QY 661 gttgatcgaagtagaagtaggttaaacagcggtcttacttrttaagtgaacttatcaagtggc 720  
|||||  
Db 661 GTTGATCAAGTAGAAGTAGTAAAGCAAGCGGCTTACTTTRTTAAGTGACTTATCAAGTGGC 720  
|||||  
QY 721 gttacagtgaaataattattcatgtagatgagcggtattccacgaataataaa 771  
|||||  
Db 721 GTTACAGTGAAATATTTTCATGTAGATAGCGGATTCACGCAATTAATAAA 771  
|||||

## RESULT 7

PCT-US00-29451-11  
; Sequence 11, Application PC/TUS0029451  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM P.L.C.  
; TITLE OF INVENTION: METHODS FOR MAKING AND USING FATTY ACID  
; TITLE OF INVENTION: SYNTHESIS PATHWAY REAGENTS  
; FILE REFERENCE: CM50068  
; CURRENT APPLICATION NUMBER: PCT/US00/29451  
; CURRENT FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: 60/161,775  
; PRIOR FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
PCT-US00-29451-11

Query Match 99.6%; Score 767.6; DB 1; Length 774;  
Best Local Similarity 100.0%; Pred. No. 9.6e-177;  
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ttaaatcttgaaacaaacatatgtcatatggtggaatcgctaatgaagcgtagtattgct 63  
|||||  
Db 7 ttaaatcttgaaacaaacatatgtcatatggtggaatcgctaatgaagcgtagtattgct 66  
|||||  
QY 64 ttgtgtgctgtaagtttttagatcaatttaggtgctaaatagttatttacttaccgtaaa 123  
|||||  
Db 67 ttgtgtgctgtaagtttttagatcaatttaggtgctaaatagttatttacttaccgtaaa 126  
|||||  
QY 124 gaacgtgacgtgaagagcttgaaataattattagaacaataataacaccagaagcgac 183  
|||||  
Db 127 gaacgtgacgtgaagagcttgaaataattattagaacaataataacaccagaagcgac 186  
|||||  
QY 184 ttatatcaattgattgttcaaacgcatgaagaggttatttaattggtttttgagcaaatggt 243  
|||||

Db 187 ttatatcaattgattgttcaaacgcatgaagaggttatttaattggttttgagcaaatggt 246  
|||||  
QY 244 aaagatgttgcaaatatttgatggtgtatatcatccaacgcgcatcttgctaaatagaaac 303  
|||||  
Db 247 aaagatgttgcaaatatttgatggtgtatatcatccaacgcgcatcttgctaaatagaaac 306  
|||||  
QY 304 ttacgagacgctttctgaaacttcaagtggaaggtctctgttagctcaagacattagt 363  
|||||  
Db 307 ttacgagacgctttctgaaacttcaagtggaaggtctctgttagctcaagacattagt 366  
|||||  
QY 364 tcttactcattcaacaatttggtgctcaatgaagctaaaaaataatgaagcgaaggtggtgac 423  
|||||  
Db 367 tcttactcattcaacaatttggtgctcaatgaagctaaaaaataatgaagcgaaggtggtgac 426  
|||||  
QY 424 attgttgcaacaacataatttaggtggtgcaaatccagattccagattcaataatgtagtgggt 483  
|||||  
Db 427 attgttgcaacaacataatttaggtggtgcaaatccagattccagattcaataatgtagtgggt 486  
|||||  
QY 484 gttgtaaacgagcgttagaagcaaatgttaaatatttagcattagcatttaggtctctgat 543  
|||||  
Db 487 gttgtaaacgagcgttagaagcaaatgttaaatatttagcattagcatttaggtctctgat 546  
|||||  
QY 544 aatattcgtgttaattgcaatttcagctggtcccaatccgtacatttaagtcgaaggtggtg 603  
|||||  
Db 547 aatattcgtgttaattgcaatttcagctggtcccaatccgtacatttaagtcgaaggtggtg 606  
|||||  
QY 604 gttggttcaatacaattcttaagaaatcgaagagcgctgcaccttttaaacgtaacgtt 663  
|||||  
Db 607 gttggttcaatacaattcttaagaaatcgaagagcgctgcaccttttaaacgtaacgtt 666  
|||||  
QY 664 gatcaagtagaagtaggtcaaacagcggtctacttrttaagtgaacttatcaagtggtgct 723  
|||||  
Db 667 gatcaagtagaagtaggtcaaacagcggtctacttrttaagtgaacttatcaagtggtgct 726  
|||||  
QY 724 acaggtgaaataattcatgtagatgagcggttccacgcgaatcaataaa 771  
|||||  
Db 727 acaggtgaaataattcatgtagatgagcggttccacgcgaatcaataaa 774  
|||||

## RESULT 8

PCT-US02-03987-8794  
; Sequence 8794, Application PC/TUS0203987  
; GENERAL INFORMATION:  
; APPLICANT: Elittra Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit  
; TITLE OF INVENTION: Proliferation  
; FILE REFERENCE: ELITRA.028VPC  
; CURRENT APPLICATION NUMBER: PCT/US02/03987  
; CURRENT FILING DATE: 2002-02-02  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 15811  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8794  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(771)  
PCT-US02-03987-8794

Query Match 98.9%; Score 762.6; DB 1; Length 771;  
Best Local Similarity 99.2%; Pred. No. 1.1e-175;  
Matches 765; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 atgttaattcttgaaacaaacatatgtcatatggtggaatcgctaatgaagcgtagtatt 60  
|||||  
Db 1 atgttaattcttgaaacaaacatatgtcatatggtggaatcgctaatgaagcgtagtatt 60  
|||||  
QY 61 gcttttggtgcgtgaagtttttagatcaaatggtgctaaattagttatttacttaacgt 120  
|||||

Db 61 gcttttggtgcgtctaaagtttagatcaatttagtgctaaatttagtatttactaccgt 120  
Qy 121 aaagaacgtgacgtctaaagagcttgaaataattattagaaacattataaatacaacagaagcg 180  
Db 121 aaagaacgtgacgtctaaagagcttgaaataattattagaaacattataaatacaacagaagcg 180  
Qy 181 cacttatatacaattgatgttccaagcgatgaagaggttatttaattggttttagcacaatt 240  
Db 181 cacttatatacaattgatgttccaagcgatgaagaggttatttaattggttttagcacaatt 240  
Qy 241 gqtaagaatgttgcaataattgatgtgtatcatcatcattcaatcgcatcttgcataatggaa 300  
Db 241 gqtaagaatgttgcaataattgatgtgtatcatcatcattcaatcgcatcttgcataatggaa 300  
Qy 301 gacttacgcggagcgttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 360  
Db 301 gacttacgcggagcgttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 360  
Qy 361 agtttactatcaataattgctctatgaagctatgaagctataaataattatgaaggtggt 420  
Db 361 agtttactatcaataattgctctatgaagctatgaagctataaataattatgaaggtggt 420  
Qy 421 acattgttgcaacaacattattagtggtgcgaattcgcagttcgaataattataatgtgag 480  
Db 421 acattgttgcaacaacattattagtggtgcgaattcgcagttcgaataattataatgtgag 480  
Qy 481 ggtgtgtctaaagcgagcttagaagcaaatgttaataatttagcattagacttagtct 540  
Db 481 ggtgtgtctaaagcgagcttagaagcaaatgttaataatttagcattagacttagtctca 540  
Qy 541 gataatattcgcgttaagtaagcaatttcagctgtgcgaattcgaataattataatgtgag 600  
Db 541 gataatattcgcgttaagtaagcaatttcagctgtgcgaattcgaataattataatgtgag 600  
Qy 601 gfggggtgttcaataacatttcataagcaatcgaagcggtgcacatttaaaacgtaac 660  
Db 601 gfggggtgttcaataacatttcataagcaatcgaagcggtgcacatttaaaacgtaac 660  
Qy 661 gttgatcaagtagaagtagttaaagcagcggtcttacttrttaagtgaacttacaagtgc 720  
Db 661 gttgatcaagtagaagtagttaaagcagcggtcttacttrttaagtgaacttacaagtgc 720  
Qy 721 gttacaggtgaaataattcatgtagatagcggattccacgcgaattataaa 771  
Db 721 gttacaggtgaaataattcatgtagatagcggattccacgcgaattataaa 771

RESULT 9

US-09-815-242-8794  
; Sequence 8794, Application US/09815242  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8794  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(771)  
US-09-815-242-8794  
  
Query Match 98.9%; Score 762.6; MB 31; Length 771;  
Best Local Similarity 99.2%; Pred. No. 1.6e-175;  
Matches 765; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 1 atgttaaatcttgaaacaaacataatgcatcatggtggaatcgctaaataagcgtatt 60  
Db 1 atgttaaatcttgaaacaaacataatgcatcatggtggaatcgctaaataagcgtatt 60  
Qy 61 gcttttggtgcgtctaaagtttagatcaatttagtgctaaatttagtatttactaccgt 120  
Db 61 gcttttggtgcgtctaaagtttagatcaatttagtgctaaatttagtatttactaccgt 120  
Qy 121 aaagaacgtgacgtctaaagagcttgaaataattattagaaacattataaatacaacagaagcg 180  
Db 121 aaagaacgtgacgtctaaagagcttgaaataattattagaaacattataaatacaacagaagcg 180  
Qy 181 cacttatatacaattgatgttcaaaacgtatgaagaggttatttaattggttttagcacaatt 240  
Db 181 cacttatatacaattgatgttcaaaacgtatgaagaggttatttaattggttttagcacaatt 240  
Qy 241 ggttaagatgttggaacattattggtgtatcatcattcaatcgcatcttgcataatggaa 300  
Db 241 ggttaagatgttggaacattattggtgtatcatcattcaatcgcatcttgcataatggaa 300  
Qy 301 gacttacgcggagcgttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 360  
Db 301 gacttacgcggagcgttttctgaaacttcacgtgaaggtcttctgttagctcaagacatt 360  
Qy 361 agtttactatcaataatttggtctcatgaagctaaataattataatgccaaggtggt 420  
Db 361 agtttactatcaataatttggtctcatgaagctaaataattataatgccaaggtggt 420  
Qy 421 agcattgttgcaacaacataatttagtggtgcgaattcgcagttcgaataattataatgtgatg 480  
Db 421 agcattgttgcaacaacataatttagtggtgcgaattcgcagttcgaataattataatgtgatg 480  
Qy 481 ggtgtgtctaaagcgagcttagaagcaaatgttataattatttagcatttagcttccct 540  
Db 481 ggtgtgtctaaagcgagcttagaagcaaatgttataattatttagcatttagcttccca 540  
Qy 541 gataatattcgcgtttaaataatttcagctgtgcgaattcgcgaattataatgcaaaaggt 600  
Db 541 gataatattcgcgtttaaataatttcagctgtgcgaattcgcgaattataatgcaaaaggt 600  
Qy 601 gfggggtgttcaataacatttcataagcaatcgaagcggtgcacatttaaaacgtaac 660  
Db 601 gfggggtgttcaataacatttcataagcaatcgaagcggtgcacatttaaaacgtaac 660  
Qy 661 gttgatcaagtagaagtagttaaagcagcggtcttacttrttaagtgaacttacaagtgc 720  
Db 661 gttgatcaagtagaagtagttaaagcagcggtcttacttrttaagtgaacttacaagtgc 720  
Qy 721 gttacaggtgaaataattcatgtagatagcggattccacgcgaattataaa 771  
Db 721 gttacaggtgaaataattcatgtagatagcggattccacgcgaattataaa 771

## RESULT 10

US-10-072-851-8794  
; Sequence 8794, Application US/10072851  
; GENERAL INFORMATION:

; APPLICANT: Carr, Grant J.  
; APPLICANT: Xu, H. Howard  
; APPLICANT: Foulkes, J. Gordon  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Roemer, Terry  
; APPLICANT: Jiang, Bo  
; APPLICANT: Boone, Charles  
; APPLICANT: Bussey, Howard

; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits  
; TITLE OF INVENTION: Proliferation  
; FILE REFERENCE: ELITRA.028A  
; CURRENT APPLICATION NUMBER: US/10/072,851  
; CURRENT FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 15811  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8794

; LENGTH: 771

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(771)

US-10-072-851-8794

Query Match 98.9%; Score 762.6; DB 37; Length 771;  
Best Local Similarity 99.2%; Pred. No. 1.6e-175;  
Matches 765; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 atgttaaatcttgaaacaaacataatgtcatcatgtggaatcgtaataagcgtagtatt 60  
Db 1 atgttaaatcttgaaacaaacataatgtcatcatgtggaatcgtaataagcgtagtatt 60  
Qy 61 gcttttggtgcgctaagtttagatcaattaggtgctaaattagttatttactaccgt 120  
Db 61 gcttttggtgcgctaagtttagatcaattaggtgctaaattagttatttactaccgt 120  
Qy 121 aaagaacgtagccgtaaaagcgttgaaatatttagaacaattaaatcaaccagaagcg 180  
Db 121 aaagaacgtagccgtaaaagcgttgaaatatttagaacaattaaatcaaccagaagcg 180  
Qy 181 cacttatcaaatattgatgttcaaaagcgtgaagaggttatttaattgtttgcaaat 240  
Db 181 cacttatcaaatattgatgttcaaaagcgtgaagaggttatttaattgtttgcaaat 240  
Qy 241 ggtaaaagatgttgcaaatattgatgttcaaaagcgtgaagaggttatttaattgtttgcaaat 300  
Db 241 ggtaaaagatgttgcaaatattgatgttcaaaagcgtgaagaggttatttaattgtttgcaaat 300  
Qy 301 gacttacgcggaagcgttttctgaaacttcacgtgaagcgttctgttagctcaagacatt 360  
Db 301 gacttacgcggaagcgttttctgaaacttcacgtgaagcgttctgttagctcaagacatt 360  
Qy 361 agttcttactcatcaacaattgtggtcatgaagcgtcaaaaatttaagccagaagtggt 420  
Db 361 agttcttactcatcaacaattgtggtcatgaagcgtcaaaaatttaagccagaagtggt 420  
Qy 421 agcattgttgcacaaacataatttaggtggcggaattcgcagttcaaaaatttaagccagaagtggt 480  
Db 421 agcattgttgcacaaacataatttaggtggcggaattcgcagttcaaaaatttaagccagaagtggt 480

Db 421 agcattgttgcacaaacataatttaggtggcggaattcgcagttcaaaaatttaagtgatg 480  
Qy 481 ggtgtgtctaaagcgagcttagaagcaaatgttaaatatttagcattagacttaggtcct 540  
Db 481 ggtgtgtctaaagcgagcttagaagcaaatgttaaatatttagcattagacttaggtcct 540  
Qy 541 gataatattcgcgttaattgcaatttcagctggtcccaatccgtacatttaagtgcaaaaggt 600  
Db 541 gataatattcgcgttaattgcaatttcagctggtcccaatccgtacatttaagtgcaaaaggt 600  
Qy 601 gtgggtgtttcaatacaaatcttaaaagaaatcgaaagagcgtgcaccttttaaaacgtaac 660  
Db 601 gtgggtgtttcaatacaaatcttaaaagaaatcgaaagagcgtgcaccttttaaaacgtaac 660  
Qy 661 gttgatcaagtagaagtaggttaaaacagcggtctacttrttaagtacattatcaagtgcc 720  
Db 661 gttgatcaagtagaagtaggttaaaacagcggtctacttrttaagtacattatcaagtgcc 720  
Qy 721 gttacaggtgaaaatattcatgtatagatgcggtatccacgcgaattaaataa 771  
Db 721 gttacaggtgaaaatattcatgtatagatgcggtatccacgcgaattaaataa 771

## RESULT 11

PCT-US99-19726-5

; Sequence 5, Application PC/TUS9919726

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides

; FILE REFERENCE: PB484

; CURRENT APPLICATION NUMBER: PCT/US99/19726

; CURRENT FILING DATE: 1999-08-31

; EARLIER APPLICATION NUMBER: 60/098,964

; EARLIER FILING DATE: 1998-09-01

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 916

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

PCT-US99-19726-5

Query Match 98.7%; Score 761; DB 1; Length 916;  
Best Local Similarity 99.1%; Pred. No. 4.1e-175;  
Matches 764; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 atgttaaatcttgaaacaaacataatgtcatcatgtggaatcgtaataagcgtagtatt 60  
Db 96 atgttaaatcttgaaacaaacataatgtcatcatgtggaatcgtaataagcgtagtatt 155  
Qy 61 gcttttggtgcgctaagtttagatcaattaggtgctaaattagttatttactaccgt 120  
Db 156 gcttttggtgcgctaagtttagatcaattaggtgctaaattagttatttactaccgt 215  
Qy 121 aaagaacgtagccgtaaaagcgttgaaatatttagaacaattaaatcaaccagaagcg 180  
Db 216 aaagaacgtagccgtaaaagcgttgaaatatttagaacaattaaatcaaccagaagcg 275  
Qy 181 cacttatcaaatattgatgttcaaaagcgtgaagaggttatttaattgtttgcaaat 240  
Db 276 cacttatcaaatattgatgttcaaaagcgtgaagaggttatttaattgtttgcaaat 335  
Qy 241 ggtaaaagatgttgcaaatattgatgttcaaaagcgtgaagaggttatttaattgtttgcaaat 300  
Db 336 ggtaaaagatgttgcaaatattgatgttcaaaagcgtgaagaggttatttaattgtttgcaaat 395  
Qy 301 gacttacgcggaagcgttttctgaaacttcacgtgaagcgttctgttagctcaagacatt 360  
Db 396 gacttacgcggaagcgttttctgaaacttcacgtgaagcgttctgttagctcaagacatt 455  
Qy 361 agttcttactcatcaacaatttaggtggcggaattcgcagttcaaaaatttaagccagaagtggt 420  
Db 361 agttcttactcatcaacaatttaggtggcggaattcgcagttcaaaaatttaagccagaagtggt 420





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Db 216 aaagaacgtagcgttaagagagcgttgaataattattagaaacatttaatacaacacagaagcg 275
QY 181 cacttatatacaattgatgttcaagcgatgaagaggttatttaattggtttgagcaaat 240
Db 276 cacttatatacaattgatgttcaagcgatgaagaggttatttaattggtttgagcaaat 335
QY 241 ggttaagatgttggcaataattgatgttatatacatcaatcgacatttgcctaataatgaa 300
Db 336 ggttaagatgttggcaataattgatgttatatacatcaatcgacatttgcctaataatgaa 395
QY 301 gacttacgcggagcgttttctgaacttcacgtgaagccttctttagttagtcaagacatt 360
Db 396 gacttacgcggagcgttttctgaacttcacgtgaagccttctttagttagtcaagacatt 455
QY 361 agttcttactcaataattggtcgtcatgaagctaaataatttaataatgcagaagtggt 420
Db 456 agttcttactcaataattggtcgtcatgaagctaaataatttaataatgcagaagtggt 515
QY 421 agcattgttgcaaacataatttagtggcgaaattcgaggttcaataataataatgtgatg 480
Db 516 agcattgttgcaaacataatttagtggcgaaattcgaggttcaataataataatgtgatg 575
QY 481 ggtgtgtcgaagcgagcttagaagcaaatgttaaatatttagcatttagacttagtct 540
Db 576 ggtgtgtcgaagcgagcttagaagcaaatgttaaatatttagcatttagacttagtct 635
QY 541 gataatattcgcgttaattgaatttcagctggttccaaatccgtacatttaagtgcagaaggt 600
Db 636 gataatattcgcgttaattgaatttcagctggttccaaatccgtacatttaagtgcagaaggt 695
QY 601 ggggtgttccaaatcacatttcttaaaagaataatcgagagcgtgcacctttaaagcgtaac 660
Db 696 ggggtgttccaaatcacatttcttaaaagaataatcgagagcgtgcacctttaaagcgtaac 755
QY 661 gttgatcaagtagaagtaggtaaaacagcggcttacttirtaagtgcattcatcaagtgcg 720
Db 756 gttgatcaagtagaagtaggtaaaacagcggcttacttirtaagtgcattcatcaagtgcg 815
QY 721 gttacaggtgaaatattcatgtatagcgggattccacgcaataataaa 771
Db 816 gttacaggtgaaatattcatgtatagcgggattccacgcaataataaa 866

RESULT 14
PCT-US00-12104-1
; Sequence 1, Application PC/TUS0012104
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS
; TITLE OF INVENTION: MODULATING FAB I ACTIVITY
; FILE REFERENCE: GM50056
; CURRENT APPLICATION NUMBER: PCT/US00/12104
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 775
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
PCT-US00-12104-1

Query Match 98.1%; Score 756.6; DB 1; Length 775;
Best Local Similarity 99.5%; Pred. No. 4.6e-174;
Matches 771; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 atgttaaatcttgaatacaataatgtcatctatggtggaatcgtaataagcgtagtatt 60
Db 1 atgttaaatcttgaatacaataatgtcatctatggtggaatcgtaataagcgtagtatt 60
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QY 61 gcttttggctgcgttaaggttttagatcaattaggctgctaaatttagtatttaccgt 120
Db 61 gcttttggctgcgttaaggttttagatcaattaggctgctaaatttagtatttaccgt 120
QY 121 aaagaacgtagcgttaagagcgttgaataattattagaacatttaatacaacagaagcg 180
Db 121 aaagaacgtagcgttaagagcgttgaataattattagaacatttaatacaacagaagcg 180
QY 181 cacttatatacaattgatgttcaagcgatgaagaggttatttaattggtttgagcaaat 240
Db 181 cacttatatacaattgatgttcaagcgatgaagaggttatttaattggtttgagcaaat 240
QY 241 ggttaagatgttggcaataattgatgttatatacatcaatcgacatttgcctaataatgaa 300
Db 241 ggttaagatgttggcaataattgatgttatatacatcaatcgacatttgcctaataatgaa 300
QY 301 gacttacgcggagcgttttctgaacttcacgtgaagccttctttagttagtcaagacatt 360
Db 301 gacttacgcggagcgttttctgaacttcacgtgaagccttctttagttagtcaagacatt 360
QY 361 agttcttactcaataattggtcgtcatgaagctaaataatttaataatgcagaagtggt 420
Db 361 agttcttactcaataattggtcgtcatgaagctaaataatttaataatgcagaagtggt 420
QY 421 agcattgttgcaaacataatttagtggcgaaattcgaggttcaataataataatgtgatg 480
Db 421 agcattgttgcaaacataatttagtggcgaaattcgaggttcaataataataatgtgatg 480
QY 481 ggtgtgtcgaagcgagcttagaagcaaatgttaaatatttagcatttagacttagtct 540
Db 481 ggtgtgtcgaagcgagcttagaagcaaatgttaaatatttagcatttagacttagtct 540
QY 541 gataatattcgcgttcaattgaatttcagctggttccaaatccgtacatttaagtgcagaaggt 600
Db 541 gataatattcgcgttcaattgaatttcagctggttccaaatccgtacatttaagtgcagaaggt 600
QY 601 ggggtgttccaaatcacatttcttaaaagaataatcgagagcgtgcacctttaaagcg 656
Db 601 ggggtgttccaaatcacatttcttaaaagaataatcgagagcgtgcacctttaaagcg 660
QY 657 taagcgttagcaagtagaagtaggtaaaacagcggcttacttirtaagtgcattcatcaag 716
Db 661 taagcgttagcaagtagaagtaggtaaaacagcggcttacttirtaagtgcattcatcaag 720
QY 717 tggcgttacaggtgaaatattcatgtatagcgggattccacgcaataataaa 771
Db 721 tggcgttacaggtgaaatattcatgtatagcgggattccacgcaataataaa 775

RESULT 15
US-10-009-219-1
; Sequence 1, Application US/10009219
; GENERAL INFORMATION:
; APPLICANT: DEWOLF, WALTER E.
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS
; TITLE OF INVENTION: MODULATING FAB I ACTIVITY
; FILE REFERENCE: GM50056
; CURRENT APPLICATION NUMBER: US/10/009,219
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PCT/US00/12104
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/134,362
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 775
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-009-219-1

Query Match 98.1%; Score 756.6; DB 37; Length 775;
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